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(54) Title: *CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING PROTEINS INVOLVED IN CARBON METABOLISM AND ENERGY PRODUCTION

(57) Abstract: Isolated nucleic acid molecules, designated SMP nucleic acid molecules, which encode novel SMP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing SMP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated SMP proteins, mutated SMP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of SMP genes in this organism.

CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN CARBON METABOLISM AND ENERGY PRODUCTION

Related Applications

This application claims priority to prior U.S. Provisional Patent Application Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application Serial No. 60/143208, filed July 9, 1999, and U.S. Provisional Patent Application Serial No. 60/151572, filed August 31, 1999. This application also claims priority to prior German Patent Application No. 19931412.8, filed July 8, 1999, German Patent Application No. 19931413.6, filed July 8, 1999, German Patent Application No. 19931419.5, filed July 8, 1999, German Patent Application No. 19931420.9, filed July 8, 1999, German Patent Application No. 19931424.1, filed July 8, 1999, German Patent Application No. 19931428.4, filed July 8, 1999, German Patent Application No. 19931431.4, filed July 8, 1999, German Patent Application No. 19931433.0, filed July 8, 1999, German Patent Application No. 19931434.9, filed July 8, 1999, German Patent Application No. 19931510.8, filed July 8, 1999, German Patent Application No. 19931562.0, filed July 8, 1999, German Patent Application No. 19931634.1, filed July 8, 1999, German Patent Application No. 19932180.9, filed July 9, 1999, German Patent Application No. 19932227.9, filed July 9, 1999, German Patent Application No. 19932230.9, filed July 9, 1999, German Patent Application No. 19932924.9, filed July 14, 1999, German Patent Application No. 19932973.7, filed July 14, 1999, German Patent Application No. 19933005.0, filed July 14, 1999, German Patent Application No. 19940765.7, filed August 27, 1999, German Patent Application No. 19942076.9, filed September 3, 1999, German Patent Application No. 19942079.3, filed September 3, 1999, German Patent Application No. 19942086.6, filed September 3, 1999, German Patent Application No. 19942087.4, filed September 3, 1999, German Patent Application No. 19942088.2, filed September 3, 1999, German Patent Application No. 19942095.5, filed September 3, 1999, German Patent Application No. 19942123.4, filed September 3, 1999, and German Patent Application No. 19942125.0, filed September 3, 1999. The entire contents of all of the aforementioned application are hereby expressly incorporated herein by this reference.

Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as sugar metabolism and oxidative phosphorylation (SMP) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The SMP nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by fermentation processes. Modulation of the expression of the SMP nucleic acids of the invention, or modification of the sequence of the SMP nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a

microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a Corynebacterium or Brevibacterium species).

The SMP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The SMP nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered Corynebacterium or Brevibacterium species.

The SMP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama et al, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals. This improved production or efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation.

There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and $FADH_2$ to compounds containing high energy phosphate bonds via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) Biology of Prokaryotes, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least

due to the presence of a greater number of viable cells, each producing the desired fine chemical. Also, many of the degradation products produced during sugar metabolism are utilized by the cell as precursors or intermediates in the production of other desirable products, such as fine chemicals. So, by increasing the ability of the cell to metabolize sugars, the number of these degradation products available to the cell for other processes should also be increased.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as SMP proteins, which are capable of, for example, performing a function involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Nucleic acid molecules encoding an SMP protein are referred to herein as SMP nucleic acid molecules. In a preferred embodiment, the SMP protein participates in the conversion of carbon molecules and degradation products thereof to energy which is utilized by the cell for metabolic processes. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an SMP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of SMP-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ

ID NO:6, SEQ ID NO:8....).. The preferred SMP proteins of the present invention also preferably possess at least one of the SMP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an SMP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown in the corresponding odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an SMP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and is able to perform a function involved in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO in the Sequence Listing) A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* SMP protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an SMP protein by culturing the host cell in a suitable medium. The SMP protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an SMP gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated SMP sequence as a transgene. In another embodiment, an endogenous SMP gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered SMP gene. In another embodiment, an endogenous or introduced SMP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SMP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SMP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SMP gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Cornyebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the

sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 782) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated SMP protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated SMP protein or portion thereof is capable of performing a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In another preferred embodiment, the isolated SMP protein or portion thereof is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*.

The invention also provides an isolated preparation of an SMP protein. In preferred embodiments, the SMP protein comprises an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated SMP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated SMP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98,%, or 99% or more homologous to a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred that the preferred forms of SMP proteins also have one or more of the SMP bioactivities described herein.

The SMP polypeptide, or a biologically active portion thereof, can be operatively linked to a non-SMP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the SMP protein alone. In other preferred embodiments, this fusion protein performs a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an SMP protein, either by interacting with the protein itself or a substrate or binding partner of the SMP protein, or by modulating the transcription or translation of an SMP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an SMP nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an SMP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an

agent which modulates SMP protein activity or SMP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* carbon metabolism pathways or for the production of energy through processes such as oxidative phosphorylation, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates SMP protein activity can be an agent which stimulates SMP protein activity or SMP nucleic acid expression. Examples of agents which stimulate SMP protein activity or SMP nucleic acid expression include small molecules, active SMP proteins, and nucleic acids encoding SMP proteins that have been introduced into the cell. Examples of agents which inhibit SMP activity or expression include small molecules and antisense SMP nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant SMP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides SMP nucleic acid and protein molecules which are involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where overexpression or optimization of a glycolytic pathway protein has a direct impact on the yield, production, and/or efficiency of production of, *e.g.*, pyruvate from modified *C. glutamicum*), or may have an indirect

impact which nonetheless results in an increase of yield, production, and/or efficiency of production of the desired compound (*e.g.*, where modulation of proteins involved in oxidative phosphorylation results in alterations in the amount of energy available to perform necessary metabolic processes and other cellular functions, such as nucleic acid and protein biosynthesis and transcription/translation). Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. *Amino Acid Metabolism and Uses*

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-

recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino aids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others

described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α-ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β-carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own

production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological

Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B_1) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B_2) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B_6' (*e.g.*, pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)-β-alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β-alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β-alanine and for the condensation to panthotenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of panthothante, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B_5), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α-ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B_{12}) and porphyrines belong to a group of chemicals characterized by a tetrapyrole ring system.

The biosynthesis of vitamin B_{12} is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B_6, pantothenate, and biotin. Only Vitamin B_{12} is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of

enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) Nucleotides and Related Compounds in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: Progress in Nucleic Acid Research and Molecular Biology, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α, α-1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) J. Japan 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Sugar and Carbon Molecule Utilization and Oxidative Phosphorylation

Carbon is a critically important element for the formation of all organic compounds, and thus is a nutritional requirement not only for the growth and division of *C. glutamicum*, but also for the overproduction of fine chemicals from this microorganism. Sugars, such as mono-, di-, or polysaccharides, are particularly good carbon sources, and thus standard growth media typically contain one or more of: glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch, or cellulose (Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes", VCH: Weinheim). Alternatively, more complex forms of sugar may be utilized in the media, such as molasses, or other by-products of sugar refinement. Other compounds aside from the sugars may be used as alternate carbon sources, including alcohols (*e.g.*, ethanol or methanol), alkanes, sugar alcohols, fatty acids, and organic acids (*e.g.*, acetic acid or lactic acid). For a review of carbon sources and their utilization by microorganisms in culture, see: Ullman's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes", VCH: Weinheim; Stoppok, E. and Buchholz, K. (1996) "Sugar-based raw materials for fermentation applications" in Biotechnology (Rehm, H.J. *et al.*, eds.) vol. 6, VCH: Weinheim, p. 5-29; Rehm, H.J. (1980) Industrielle Mikrobiologie, Springer: Berlin; Bartholomew, W.H., and Reiman, H.B. (1979). Economics of Fermentation Processes, in: Peppler, H.J. and Perlman, D., eds. Microbial Technology 2nd ed., vol. 2, chapter 18, Academic Press: New York; and

Kockova-Kratachvilova, A. (1981) Characteristics of Industrial Microorganisms, in: Rehm, H.J. and Reed, G., eds. Handbook of Biotechnology, vol. 1, chapter 1, Verlag Chemie: Weinheim.

After uptake, these energy-rich carbon molecules must be processed such that they are able to be degraded by one of the major sugar metabolic pathways. Such pathways lead directly to useful degradation products, such as ribose-5-phosphate and phosphoenolpyruvate, which may be subsequently converted to pyruvate. Three of the most important pathways in bacteria for sugar metabolism include the Embden-Meyerhoff-Pamas (EMP) pathway (also known as the glycolytic or fructose bisphosphate pathway), the hexosemonophosphate (HMP) pathway (also known as the pentose shunt or pentose phosphate pathway), and the Entner-Doudoroff (ED) pathway (for review, see Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York, and Stryer, L. (1988) Biochemistry, Chapters 13-19, Freeman: New York, and references therein).

The EMP pathway converts hexose molecules to pyruvate, and in the process produces 2 molecules of ATP and 2 molecules of NADH. Starting with glucose-1-phosphate (which may be either directly taken up from the medium, or alternatively may be generated from glycogen, starch, or cellulose), the glucose molecule is isomerized to fructose-6-phosphate, is phosphorylated, and split into two 3-carbon molecules of glyceraldehyde-3-phosphate. After dehydrogenation, phosphorylation, and successive rearrangements, pyruvate results.

The HMP pathway converts glucose to reducing equivalents, such as NADPH, and produces pentose and tetrose compounds which are necessary as intermediates and precursors in a number of other metabolic pathways. In the HMP pathway, glucose-6-phosphate is converted to ribulose-5-phosphate by two successive dehydrogenase reactions (which also release two NADPH molecules), and a carboxylation step. Ribulose-5-phosphate may also be converted to xyulose-5-phosphate and ribose-5-phosphate; the former can undergo a series of biochemical steps to glucose-6-phosphate, which may enter the EMP pathway, while the latter is commonly utilized as an intermediate in other biosynthetic pathways within the cell.

The ED pathway begins with the compound glucose or gluconate, which is subsequently phosphorylated and dehydrated to form 2-dehydro-3-deoxy-6-P-gluconate.

Glucuronate and galacturonate may also be converted to 2-dehydro-3-deoxy-6-P-gluconate through more complex biochemical pathways. This product molecule is subsequently cleaved into glyceraldehyde-3-P and pyruvate; glyceraldehyde-3-P may itself also be converted to pyruvate.

The EMP and HMP pathways share many features, including intermediates and enzymes. The EMP pathway provides the greatest amount of ATP, but it does not produce ribose-5-phosphate, an important precursor for, *e.g.*, nucleic acid biosynthesis, nor does it produce erythrose-4-phosphate, which is important for amino acid biosynthesis. Microorganisms that are capable of using only the EMP pathway for glucose utilization are thus not able to grow on simple media with glucose as the sole carbon source. They are referred to as fastidious organisms, and their growth requires inputs of complex organic compounds, such as those found in yeast extract.

In contrast, the HMP pathway produces all of the precursors necessary for both nucleic acid and amino acid biosynthesis, yet yields only half the amount of ATP energy that the EMP pathway does. The HMP pathway also produces NADPH, which may be used for redox reactions in biosynthetic pathways. The HMP pathway does not directly produce pyruvate, however, and thus these microorganisms must also possess this portion of the EMP pathway. It is therefore not surprising that a number of microorganisms, particularly the facultative anerobes, have evolved such that they possess both of these pathways.

The ED pathway has thus far has only been found in bacteria. Although this pathway is linked partly to the HMP pathway in the reverse direction for precursor formation, the ED pathway directly forms pyruvate by the aldolase cleavage of 3-ketodeoxy-6-phosphogluconate. The ED pathway can exist on its own and is utilized by the majority of strictly aerobic microorganisms. The net result is similar to that of the HMP pathway, although one mole of ATP can be formed only if the carbon atoms are converted into pyruvate, instead of into precursor molecules.

The pyruvate molecules produced through any of these pathways can be readily converted into energy via the Krebs cycle (also known as the citric acid cycle, the citrate cycle, or the tricarboxylic acid cycle (TCA cycle)). In this process, pyruvate is first decarboxylated, resulting in the production of one molecule of NADH, 1 molecule of acetyl-CoA, and 1 molecule of CO_2. The acetyl group of acetyl CoA then reacts with

the 4 carbon unit, oxaolacetate, leading to the formation of citric acid, a 6 carbon organic acid. Dehydration and two additional CO_2 molecules are released. Ultimately, oxaloacetate is regenerated and can serve again as an acetyl acceptor, thus completing the cycle. The electrons released during the oxidation of intermediates in the TCA cycle are transferred to NAD^+ to yield NADH.

During respiration, the electrons from NADH are transferred to molecular oxygen or other terminal electron acceptors. This process is catalyzed by the respiratory chain, an electron transport system containing both integral membrane proteins and membrane associated proteins. This system serves two basic functions: first, to accept electrons from an electron donor and to transfer them to an electron acceptor, and second, to conserve some of the energy released during electron transfer by the synthesis of ATP. Several types of oxidation-reduction enzymes and electron transport proteins are known to be involved in such processes, including the NADH dehydrogenases, flavin-containing electron carriers, iron sulfur proteins, and cytochromes. The NADH dehydrogenases are located at the cytoplasmic surface of the plasma membrane, and transfer hydrogen atoms from NADH to flavoproteins, in turn accepting electrons from NADH. The flavoproteins are a group of electron carriers possessing a flavin prosthetic group which is alternately reduced and oxidized as it accepts and transfers electrons. Three flavins are known to participate in these reactions: riboflavin, flavin-adenine dinucleotide (FAD) and flavin-mononucleotide (FMN). Iron sulfur proteins contain a cluster of iron and sulfur atoms which are not bonded to a heme group, but which still are able to participate in dehydration and rehydration reactions. Succinate dehydrogenase and aconitase are exemplary iron-sulfur proteins; their iron-sulfur complexes serve to accept and transfer electrons as part of the overall electron-transport chain. The cytochromes are proteins containing an iron porphyrin ring (heme). There are a number of different classes of cytochromes, differing in their reduction potentials. Functionally, these cytochromes form pathways in which electrons may be transferred to other cytochromes having increasingly more positive reduction potentials. A further class of non-protein electron carriers is known: the lipid-soluble quinones (*e.g.*, coenzyme Q). These molecules also serve as hydrogen atom acceptors and electron donors.

The action of the respiratory chain generates a proton gradient across the cell membrane, resulting in proton motive force. This force is utilized by the cell to synthesize ATP, via the membrane-spanning enzyme, ATP synthase. This enzyme is a multiprotein complex in which the transport of H^+ molecules through the membrane results in the physical rotation of the intracellular subunits and concomitant phosphorylation of ADP to form ATP (for review, see Fillingame, R.H. and Divall, S. (1999) *Novartis Found. Symp.* 221: 218-229, 229-234).

Non-hexose carbon substrates may also serve as carbon and energy sources for cells. Such substrates may first be converted to hexose sugars in the gluconeogenesis pathway, where glucose is first synthesized by the cell and then is degraded to produce energy. The starting material for this reaction is phosphoenolpyruvate (PEP), which is one of the key intermediates in the glycolytic pathway. PEP may be formed from substrates other than sugars, such as acetic acid, or by decarboxylation of oxaloacetate (itself an intermediate in the TCA cycle). By reversing the glycolytic pathway (utilizing a cascade of enzymes different than those of the original glycolysis pathway), glucose-6-phosphate may be formed. The conversion of pyruvate to glucose requires the utilization of 6 high energy phosphate bonds, whereas glycolysis only produces 2 ATP in the conversion of glucose to pyruvate. However, the complete oxidation of glucose (glycolysis, conversion of pyruvate into acetyl CoA, citric acid cycle, and oxidative phosphorylation) yields between 36-38 ATP, so the net loss of high energy phosphate bonds experienced during gluconeogenesis is offset by the overall greater gain in such high-energy molecules produced by the oxidation of glucose.

III. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as SMP nucleic acid and protein molecules, which participate in the conversion of sugars to useful degradation products and energy (*e.g.*, ATP) in *C. glutamicum* or which may participate in the production of useful energy-rich molecules (*e.g.*, ATP) by other processes, such as oxidative phosphorylation. In one embodiment, the SMP molecules participate in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In a preferred embodiment,

the activity of the SMP molecules of the present invention to contribute to carbon metabolism or energy production in *C. glutamicum* has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the SMP molecules of the invention are modulated in activity, such that the *C. glutamicum* metabolic and energetic pathways in which the SMP proteins of the invention participate are modulated in yield, production, and/or efficiency of production, which either directly or indirectly modulates the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, "SMP protein" or "SMP polypeptide" includes proteins which are capable of performing a function involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Examples of SMP proteins include those encoded by the SMP genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "SMP gene" or "SMP nucleic acid sequence" include nucleic acid sequences encoding an SMP protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of SMP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation

products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The term "degradation product" is art-recognized and includes breakdown products of a compound. Such products may themselves have utility as precursor (starting point) or intermediate molecules necessary for the biosynthesis of other compounds by the cell. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

In another embodiment, the SMP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and $FADH_2$ to more useful forms via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of

reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) Biology of Prokaryotes, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least due to the presence of a greater number of viable cells, each producing the desired fine chemical. Further, a number of the degradation and intermediate compounds produced during sugar metabolism are necessary precursors and intermediates for other biosynthetic pathways throughout the cell. For example, many amino acids are synthesized directly from compounds normally resulting from glycolysis or the TCA cycle (*e.g.*, serine is synthesized from 3-phosphoglycerate, an intermediate in glycolysis). Thus, by increasing the efficiency of conversion of sugars to useful energy molecules, it is also possible to increase the amount of useful degradation products as well.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* SMP DNAs and the predicted amino acid sequences of the *C. glutamicum* SMP proteins are shown in the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode proteins having a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention

(*e.g.*, the sequence of an even-numbered SEQ ID NO of the Sequence Listing). As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

An SMP protein or a biologically active portion or fragment thereof of the invention can participate in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or can have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode SMP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of SMP-encoding nucleic acid (*e.g.*, SMP DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3'end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the

genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated SMP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* SMP DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO of the Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and

appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an SMP nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing , correspond to the *Corynebacterium glutamicum* SMP DNAs of the invention. This DNA comprises sequences encoding SMP proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: sequence in the Sequence Listing), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing.. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in nucleic acid sequences of the Sequence Listing.

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, or RXS number having the designation "RXA," "RXN," or "RXS" followed by 5 digits (*i.e.*, RXA01626, RXN00043, or RXS0735). Each of the nucleic acid sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, or RXS designation to eliminate confusion. The recitation "one of the odd-numbered sequences of the Sequence Listing", then, refers to any of the nucleic acid sequences in the Sequence Listing, which may also be distinguished by their differing RXA, RXN, or RXS designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an even-numbered SEQ ID NO: immediately following the corresponding nucleic acid sequence . For example, the coding region for RXA02735 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, or RXS designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequence designated

RXA00042 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXA00042, and the amino acid sequence designated RXN00043 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXN00043. The correspondence between the RXA, RXN and RXS nucleotide and amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXAdesignation. For example, SEQ ID NO:11, designated, as indicated on Table 1, as "F RXA01312", is an F-designated gene, as are SEQ ID NOs: 29, 33, and 39 (designated on Table 1 as "F RXA02803", "F RXA02854", and "F RXA01365", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the dapD gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences of the invention is one which is sufficiently complementary to one of the nucleotide sequences shown in the Sequence Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:) such that it can hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%,

87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences of the invention, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an SMP protein. The nucleotide sequences determined from the cloning of the SMP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning SMP homologues in other cell types and organisms, as well as SMP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing), an anti-sense sequence of one of these sequences, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of the invention can be used in PCR reactions to clone SMP homologues. Probes based on the SMP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an SMP protein, such as by measuring a level of an SMP-encoding

nucleic acid in a sample of cells, *e.g.*, detecting SMP mRNA levels or determining whether a genomic SMP gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the protein or portion thereof is able to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Protein members of such sugar metabolic pathways or energy producing systems, as described herein, may play a role in the production and secretion of one or more fine chemicals. Examples of such activities are also described herein. Thus, "the function of an SMP protein" contributes either directly or indirectly to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of SMP protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention(*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing).

Portions of proteins encoded by the SMP nucleic acid molecules of the invention are preferably biologically active portions of one of the SMP proteins. As used herein, the term "biologically active portion of an SMP protein" is intended to include a portion, *e.g.*, a domain/motif, of an SMP protein that participates in the metabolism of carbon

compounds such as sugars, or in energy-generating pathways in *C. glutamicum*, or has an activity as set forth in Table 1. To determine whether an SMP protein or a biologically active portion thereof can participate in the metabolism of carbon compounds or in the production of energy-rich molecules in *C. glutamicum*, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an SMP protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the SMP protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the SMP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic code and thus encode the same SMP protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (*e.g.*, an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 58% identical to the nucleotide sequence designated RXA00014 (SEQ ID NO:41),

a nucleotide sequence which is greater than and/or at least % identical to the nucleotide sequence designated RXA00195 (SEQ ID NO:399), and a nucleotide sequence which is greater than and/or at least 42% identical to the nucleotide sequence designated RXA00196 (SEQ ID NO:401). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* SMP nucleotide sequences set forth in the Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by those of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of SMP proteins may exist within a population (*e.g.*, the *C. glutamicum* population). Such genetic polymorphism in the SMP gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an SMP protein, preferably a *C. glutamicum* SMP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the SMP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in SMP that are the result of natural variation and that do not alter the functional activity of SMP proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* SMP DNA of the invention can be isolated based on their homology to the *C. glutamicum* SMP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in

another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* SMP protein.

In addition to naturally-occurring variants of the SMP sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of the invention, thereby leading to changes in the amino acid sequence of the encoded SMP protein, without altering the functional ability of the SMP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the SMP proteins (*e.g.*, an even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said SMP protein, whereas an "essential" amino acid residue is required for SMP protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only

semi-conserved in the domain having SMP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering SMP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding SMP proteins that contain changes in amino acid residues that are not essential for SMP activity. Such SMP proteins differ in amino acid sequence from a sequence of an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the SMP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the invention and is capable of participate in the metabolism of carbon compounds such as sugars, or in the biosynthesis of high-energy compounds in *C. glutamicum*, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-70% homologous to one of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of these sequences, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the amino acid sequences the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an SMP protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an SMP protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an SMP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an SMP activity described herein to identify mutants that retain SMP activity. Following mutagenesis of the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding SMP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or

complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire SMP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an SMP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of NO. 3 (RXA01626) comprises nucleotides 1 to 345). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding SMP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding SMP disclosed herein (*e.g.*, the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of SMP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of SMP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of SMP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-

galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an SMP protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-

methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave SMP mRNA transcripts to thereby inhibit translation of SMP mRNA. A ribozyme having specificity for an SMP-encoding nucleic acid can be designed based upon the nucleotide sequence of an SMP cDNA disclosed herein (*i.e.*, SEQ ID NO. 3 (RXA01626)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an SMP-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, SMP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, SMP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an SMP nucleotide sequence (*e.g.*, an SMP promoter and/or enhancers) to form triple helical structures that prevent transcription of an SMP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an SMP protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of

autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as cos-, tac-, trp-, tet-, trp-tet-, lpp-, lac-, lpp-lac-, lacI^q-, T7-, T5-, T3-, gal-, trc-, ara-, SP6-, arny, SPO2, λ-P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MFα, AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV/35S, SSU, OCS, lib4,

usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by those of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, SMP proteins, mutant forms of SMP proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of SMP proteins in prokaryotic or eukaryotic cells. For example, SMP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* –mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion

expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the SMP protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant SMP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315), pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λgt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming Streptomyces, while plasmids pUB110, pC194, or pBD214 are suited for transformation of Bacillus species. Several plasmids of use in the transfer of genetic information into Corynebacterium include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the SMP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ, pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York (IBSN 0 444 904018).

Alternatively, the SMP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the SMP proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+,

pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018). .

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α-fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in

a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to SMP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an SMP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to one of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid,

transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an SMP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an SMP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the SMP gene. Preferably, this SMP gene is a *Corynebacterium glutamicum* SMP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous SMP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous SMP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous SMP protein). In the homologous recombination vector, the altered portion of the SMP gene is flanked at its 5' and 3' ends by additional nucleic acid of the SMP gene to allow for homologous recombination to occur between the exogenous SMP gene carried by the vector and an endogenous SMP gene in a microorganism. The additional

flanking SMP nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced SMP gene has homologously recombined with the endogenous SMP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an SMP gene on a vector placing it under control of the lac operon permits expression of the SMP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous SMP gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced SMP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SMP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SMP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SMP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described SMP gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an SMP protein. Accordingly, the invention further provides methods for producing SMP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an SMP protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered SMP protein) in a suitable medium until SMP protein is produced. In another

embodiment, the method further comprises isolating SMP proteins from the medium or the host cell.

C. Isolated SMP Proteins

Another aspect of the invention pertains to isolated SMP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of SMP protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of SMP protein having less than about 30% (by dry weight) of non-SMP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-SMP protein, still more preferably less than about 10% of non-SMP protein, and most preferably less than about 5% non-SMP protein. When the SMP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of SMP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of SMP protein having less than about 30% (by dry weight) of chemical precursors or non-SMP chemicals, more preferably less than about 20% chemical precursors or non-SMP chemicals, still more preferably less than about 10% chemical precursors or non-SMP chemicals, and most preferably less than about 5% chemical precursors or non-SMP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the SMP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* SMP protein in a microorganism such as *C. glutamicum.*

An isolated SMP protein or a portion thereof of the invention can participate in the metabolism of carbon compounds such as sugars, or in the production of energy compounds (*e.g.*, by oxidative phosphorylation) utilized to drive unfavorable metabolic pathways, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an SMP protein of the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing. In yet another preferred embodiment, the SMP protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the SMP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred SMP proteins of the present invention also preferably possess at least one of the SMP activities described herein. For example, a preferred SMP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention, and

which can perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or which has one or more of the activities set forth in Table 1.

In other embodiments, the SMP protein is substantially homologous to an amino acid sequence of of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing)and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the SMP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which has at least one of the SMP activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention.

Biologically active portions of an SMP protein include peptides comprising amino acid sequences derived from the amino acid sequence of an SMP protein, *e.g.*, an amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the amino acid sequence of a protein homologous to an SMP protein, which include fewer amino acids than a full length SMP protein or the full length protein which is homologous to an SMP protein, and exhibit at least one activity of an SMP protein. Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an SMP protein. Moreover, other

biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an SMP protein include one or more selected domains/motifs or portions thereof having biological activity.

SMP proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the SMP protein is expressed in the host cell. The SMP protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an SMP protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native SMP protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-SMP antibody, which can be produced by standard techniques utilizing an SMP protein or fragment thereof of this invention.

The invention also provides SMP chimeric or fusion proteins. As used herein, an SMP "chimeric protein" or "fusion protein" comprises an SMP polypeptide operatively linked to a non-SMP polypeptide. An "SMP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an SMP protein, whereas a "non-SMP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the SMP protein, *e.g.*, a protein which is different from the SMP protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the SMP polypeptide and the non-SMP polypeptide are fused in-frame to each other. The non-SMP polypeptide can be fused to the N-terminus or C-terminus of the SMP polypeptide. For example, in one embodiment the fusion protein is a GST-SMP fusion protein in which the SMP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant SMP proteins. In another embodiment, the fusion protein is an SMP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of an SMP protein can be increased through use of a heterologous signal sequence.

Preferably, an SMP chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, Ausubel *et al.*, eds. John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An SMP-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the SMP protein.

Homologues of the SMP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the SMP protein. As used herein, the term "homologue" refers to a variant form of the SMP protein which acts as an agonist or antagonist of the activity of the SMP protein. An agonist of the SMP protein can retain substantially the same, or a subset, of the biological activities of the SMP protein. An antagonist of the SMP protein can inhibit one or more of the activities of the naturally occurring form of the SMP protein, by, for example, competitively binding to a downstream or upstream member of the sugar molecule metabolic cascade or the energy-producing pathway which includes the SMP protein.

In an alternative embodiment, homologues of the SMP protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the SMP protein for SMP protein agonist or antagonist activity. In one embodiment, a variegated library of SMP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of SMP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential SMP

sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of SMP sequences therein. There are a variety of methods which can be used to produce libraries of potential SMP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential SMP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the SMP protein coding can be used to generate a variegated population of SMP fragments for screening and subsequent selection of homologues of an SMP protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an SMP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the SMP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of SMP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the

frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify SMP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated SMP library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of SMP protein regions required for function; modulation of an SMP protein activity; modulation of the metabolism of one or more sugars; modulation of high-energy molecule production in a cell (*i.e.*, ATP, NADPH); and modulation of cellular production of a desired compound, such as a fine chemical.

The SMP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and

spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Cornyebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in the Sequence Listing) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in C. *glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The SMP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic and energy-releasing processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the

evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the SMP nucleic acid molecules of the invention may result in the production of SMP proteins having functional differences from the wild-type SMP proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an SMP protein, either by interacting with the protein itself or a substrate or binding partner of the SMP protein, or by modulating the transcription or translation of an SMP nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more SMP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the SMP protein is assessed.

There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and $FADH_2$ to more useful forms via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit

unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

Further, modulation of one or more pathways involved in sugar utilization permits optimization of the conversion of the energy contained within the sugar molecule to the production of one or more desired fine chemicals. For example, by reducing the activity of enzymes involved in, for example, gluconeogenesis, more ATP is available to drive desired biochemical reactions (such as fine chemical biosyntheses) in the cell. Also, the overall production of energy molecules from sugars may be modulated to ensure that the cell maximizes its energy production from each sugar molecule. Inefficient sugar utilization can lead to excess CO_2 production and excess energy, which may result in futile metabolic cycles. By improving the metabolism of sugar molecules, the cell should be able to function more efficiently, with a need for fewer carbon molecules. This should result in an improved fine chemical product: sugar molecule ratio (improved carbon yield), and permits a decrease in the amount of sugars that must be added to the medium in large-scale fermentor culture of such engineered *C. glutamicum.*

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum.* For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) Biology of Prokaryotes, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least

due to the presence of a greater number of viable cells, each producing the desired fine chemical.

Further, many of the degradation products produced during sugar metabolism are themselves utilized by the cell as precursors or intermediates for the production of a number of other useful compounds, some of which are fine chemicals. For example, pyruvate is converted into the amino acid alanine, and ribose-5-phosphate is an integral part of, for example, nucleotide molecules. The amount and efficiency of sugar metabolism, then, has a profound effect on the availability of these degradation products in the cell. By increasing the ability of the cell to process sugars, either in terms of efficiency of existing pathways (*e.g.*, by engineering enzymes involved in these pathways such that they are optimized in activity), or by increasing the availability of the enzymes involved in such pathways (*e.g.*, by increasing the number of these enzymes present in the cell), it is possible to also increase the availability of these degradation products in the cell, which should in turn increase the production of many different other desirable compounds in the cell (*e.g.*, fine chemicals).

The aforementioned mutagenesis strategies for SMP proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated SMP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any product produced by *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

TABLE 1: GENES IN THE APPLICATION

HMP:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1	2	RXS02735	VV0074	14576	15280	6-Phosphoglucolactonase
3	4	RXA01626	GR00452	4270	3926	L-ribulose-phosphate 4-epimerase
5	6	RXA02245	GR00654	13639	14295	RIBULOSE-PHOSPHATE 3-EPIMERASE (EC 5.1.3.1)
7	8	RXA01015	GR00290	346	5	RIBOSE 5-PHOSPHATE ISOMERASE (EC 5.3.1.6)

TCA:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
9	10	RXN01312	VV0082	20803	18785	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1)
11	12	F RXA01312	GR00380	2690	1614	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1)
13	14	RXN00231	VV0083	15484	14015	SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (EC 1.2.1.16)
15	16	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1)
17	18	RXA01535	GR00427	1354	2760	FUMARATE HYDRATASE PRECURSOR (EC 4.2.1.2)
19	20	RXA00517	GR00131	1407	2447	MALATE DEHYDROGENASE (EC 1.1.1.37) (EC 1.1.1.82)
21	22	RXA01350	GR00392	1844	2827	MALATE DEHYDROGENASE (EC 1.1.1.37)

EMB-Pathway

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
23	24	RXA02149	GR00639	17786	18754	GLUCOKINASE (EC 2.7.1.2)
25	26	RXA01814	GR00515	2571	910	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
27	28	RXN02803	VV0086	1	657	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
29	30	F RXA02803	GR00784	2	400	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
31	32	RXN03076	VV0043	1624	35	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
33	34	F RXA02854	GR10002	1588	5	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
35	36	RXA00511	GR00129	1	513	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
37	38	RXN01365	VV0091	1476	103	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
39	40	F RXA01365	GR00397	897	4	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
41	42	RXA00098	GR00014	6525	8144	GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9)
43	44	RXA01989	GR00578	1	630	GLUCOSE-6-PHOSPHATE ISOMERASE A (GPI A) (EC 5.3.1.9)
45	46	RXA00340	GR00059	1549	2694	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
47	48	RXA02492	GR00720	2201	2917	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
49	50	RXA00381	GR00082	1451	846	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
51	52	RXA02122	GR00636	6511	5813	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
53	54	RXA00206	GR00032	6171	5134	6-PHOSPHOFRUCTOKINASE (EC 2.7.1.11)
55	56	RXA01243	GR00359	2302	3261	1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56)
57	58	RXA01882	GR00538	1165	2154	1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56)
59	60	RXA01702	GR00479	1397	366	FRUCTOSE-BISPHOSPHATE ALDOLASE (EC 4.1.2.13)
61	62	RXA02258	GR00654	26451	27227	TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1)
63	64	RXN01225	VV0064	6382	4943	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
65	66	F RXA01225	GR00354	5302	6741	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE HOMOLOG
67	68	RXA02256	GR00654	23934	24935	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
69	70	RXA02257	GR00654	25155	26369	PHOSPHOGLYCERATE KINASE (EC 2.7.2.3)
71	72	RXA00235	GR00036	2365	1091	ENOLASE (EC 4.2.1.11)
73	74	RXA01093	GR00306	1552	122	PYRUVATE KINASE (EC 2.7.1.40)
75	76	RXN02675	VV0098	72801	70945	PYRUVATE KINASE (EC 2.7.1.40)
77	78	F RXA02675	GR00754	2	364	PYRUVATE KINASE (EC 2.7.1.40)
79	80	F RXA02695	GR00755	2949	4370	PYRUVATE KINASE (EC 2.7.1.40)
81	82	RXA00682	GR00179	5299	3401	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2)
83	84	RXA00683	GR00179	6440	5349	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2)
85	86	RXN00635	VV0135	22708	20972	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
87	88	F RXA02807	GR00788	88	552	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
89	90	F RXA00635	GR00167	3	923	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
91	92	RXN03044	VV0019	1391	2221	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
93	94	F RXA02852	GR00852	3	281	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
95	96	F RXA00268	GR00041	125	955	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
97	98	RXN03086	VV0049	2243	2650	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
99	100	F RXA02887	GR10022	411	4	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
101	102	RXN03043	VV0019	1	1362	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
103	104	F RXA02897	GR10039	1291	5	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
105	106	RXN03083	VV0047	88	1110	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4)
107	108	F RXA02853	GR10001	89	1495	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4)
109	110	RXA02259	GR00654	27401	30172	PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31)
111	112	RXN02326	VV0047	4500	5315	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
113	114	F RXA02326	GR00668	5338	4523	PYRUVATE CARBOXYLASE
115	116	RXN02327	VV0047	3533	4492	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
117	118	F RXA02327	GR00668	6305	5346	PYRUVATE CARBOXYLASE
119	120	RXN02328	VV0047	1842	3437	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
121	122	F RXA02328	GR00668	7783	6401	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
123	124	RXN01048	VV0079	12539	11316	MALIC ENZYME (EC 1.1.1.39)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
125	126	F RXA01048	GR00296	3	290	MALIC ENZYME (EC 1.1.1.39)
127	128	F RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
129	130	RXA02694	GR00755	1879	2820	L-LACTATE DEHYDROGENASE (EC 1.1.1.27)
131	132	RXN00296	VV0176	35763	38606	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4)
133	134	F RXA00296	GR00048	3	2837	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4)
135	136	RXA01901	GR00544	4158	5417	L-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.3)
137	138	RXN01952	VV0105	9954	11666	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
139	140	F RXA01952	GR00562	1	216	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
141	142	F RXA01955	GR00562	4611	6209	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
143	144	RXA00293	GR00047	2645	1734	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
145	146	RXN01130	VV0157	6138	5536	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
147	148	F RXA01130	GR00315	2	304	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
149	150	RXN03112	VV0085	509	6	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
151	152	F RXA01133	GR00316	568	1116	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
153	154	RXN00871	VV0127	3127	2240	IOLB PROTEIN
155	156	F RXA00871	GR00239	2344	3207	IOLB PROTEIN: D-FRUCTOSE 1,6-BISPHOSPHATE = GLYCERONE-CC PHOSPHATE + D- GLYCERALDEHYDE 3-PHOSPHATE.
157	158	RXN02829	VV0354	287	559	IOLS PROTEIN
159	160	F RXA02829	GR00816	287	562	IOLS PROTEIN
161	162	RXN01468	VV0019	7474	8298	NAGD PROTEIN
163	164	F RXA01468	GR00422	1250	2074	PUTATIVE N-GLYCERALDEHYDE-2-PHOSPHOTRANSFERASE
165	166	RXA00794	GR00211	3993	2989	GLPX PROTEIN
167	168	RXN02920	VV0213	6135	5224	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
169	170	F RXA02379	GR00690	1390	686	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
171	172	RXN02688	VV0098	59053	58385	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
173	174	RXN03087	VV0052	3216	3428	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
175	176	RXN03186	VV0377	310	519	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
177	178	RXN03187	VV0382	3	281	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
179	180	RXN02591	VV0098	14370	12541	PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP] (EC 4.1.1.32)
181	182	RXS01260	VV0009	3477	2296	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
183	184	RXS01261	VV0009	3703	3533	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)

Glycerol metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
185	186	RXA02640	GR00749	1400	2926	GLYCEROL KINASE (EC 2.7.1.30)
187	188	RXN01025	VV0143	5483	4488	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P)+) (EC 1.1.1.94)
189	190	F RXA01025	GR00293	939	1853	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P)+) (EC 1.1.1.94)
191	192	RXA01851	GR00525	3515	1830	AEROBIC GLYCEROL-3-PHOSPHATE DEHYDROGENASE (EC 1.1.99.5)
193	194	RXA01242	GR00359	1526	2302	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR
195	196	RXA02288	GR00661	992	147	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
197	198	RXN01891	VV0122	24949	24086	GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
199	200	F RXA01891	GR00541	1736	918	GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
201	202	RXA02414	GR00703	3808	3062	Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
203	204	RXN01580	VV0122	22091	22807	Glycerophosphoryl diester phosphodiesterase

Acetate metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
205	206	RXA01436	GR00418	2547	1357	ACETATE KINASE (EC 2.7.2.1)
207	208	RXA00686	GR00179	8744	7941	ACETATE OPERON REPRESSOR
209	210	RXA00246	GR00037	4425	3391	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
211	212	RXA01571	GR00438	1360	1959	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
213	214	RXA01572	GR00438	1928	2419	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
215	216	RXA01758	GR00498	3961	2945	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
217	218	RXA02539	GR00726	11676	10159	ALDEHYDE DEHYDROGENASE (EC
219	220	RXN03061	VV0034	108	437	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
221	222	RXN03150	VV0155	10678	10055	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
223	224	RXN01340	VV0033	3	860	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
225	226	RXN01498	VV0008	1598	3160	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
227	228	RXN02674	VV0315	15614	14163	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
229	230	RXN00868	VV0127	2230	320	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
231	232	RXN01143	VV0077	9372	8254	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
233	234	RXN01146	VV0264	243	935	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
235	236	RXN01144	VV0077	8237	7722	ACETOLACTATE SYNTHASE SMALL SUBUNIT (EC 4.1.3.18)

Butanediol, diacetyl and acetoin formation

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
237	238	RXA02474	GR00715	8082	7309	(S,S)-butane-2,3-diol dehydrogenase (EC 1.1.1.76)
239	240	RXA02453	GR00710	6103	5351	ACETOIN(DIACETYL) REDUCTASE (EC 1.1.1.5)
241	242	RXS01758	VV0112	27383	28399	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)

Table 1 (continued)

HMP-Cycle

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
243	244	RXA02737	GR00763	3312	1771	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49)
245	246	RXA02738	GR00763	4499	3420	TRANSALDOLASE (EC 2.2.1.2)
247	248	RXA02739	GR00763	6769	4670	TRANSKETOLASE (EC 2.2.1.1)
249	250	RXA00965	GR00270	1232	510	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)
251	252	RXN00999	VV0106	2817	1366	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)
253	254	F RXA00999	GR00283	3012	4448	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)

Nucleotide sugar conversion

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
255	256	RXN02596	VV0098	48784	47582	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
257	258	F RXA02596	GR00742	1	489	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
259	260	F RXA02642	GR00749	5383	5880	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
261	262	RXA02572	GR00737	2	646	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22)
263	264	RXA02485	GR00718	2345	3445	UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE (EC 1.1.1.158)
265	266	RXA01216	GR00352	2302	1202	UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23)
267	268	RXA01259	GR00367	987	130	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9)
269	270	RXA02028	GR00616	573	998	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9)
271	272	RXA01262	GR00367	8351	7191	GDP-MANNOSE 6-DEHYDROGENASE (EC 1.1.1.132)
273	274	RXA01377	GR00400	3935	5020	MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13)
275	276	RXA02063	GR00626	3301	4527	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (EC 2.7.7.27)
277	278	RXN00014	VV0048	8848	9627	GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (EC 2.7.7.24)
279	280	F RXA00014	GR00002	4448	5227	GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (EC 2.7.7.24)
281	282	RXA01570	GR00438	427	1281	GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (EC 2.7.7.24)
283	284	RXA02666	GR00753	7260	6493	D-RIBITOL-5-PHOSPHATE CYTIDYLYLTRANSFERASE (EC 2.7.7.40)
285	286	RXA00825	GR00222	222	1154	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)

Inositol and ribitol metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
287	288	RXA01887	GR00539	4219	3209	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
289	290	RXN00013	VV0048	7966	8838	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3.1.3.25)
291	292	F RXA00013	GR00002	3566	4438	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3.1.3.25)
293	294	RXA01099	GR00306	6328	5504	INOSITOL MONOPHOSPHATE PHOSPHATASE
295	296	RXN01332	VV0273	579	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
297	298	F RXA01332	GR00388	552	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
299	300	RXA01632	GR00454	2338	3342	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
301	302	RXA01633	GR00454	3380	4462	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
303	304	RXN01406	VV0278	2999	1977	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
305	306	RXN01630	VV0050	48113	47037	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
307	308	RXN00528	VV0079	23406	22318	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4)
309	310	RXN03057	VV0028	7017	7688	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
311	312	F RXA02902	GR10040	10277	10948	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
313	314	RXA00251	GR00038	931	224	RIBITOL 2-DEHYDROGENASE (EC 1.1.1.56)

Utilization of sugars

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
315	316	RXN02654	VV0090	12206	13090	GLUCOSE 1-DEHYDROGENASE (EC 1.1.1.47)
317	318	F RXA02654	GR00752	7405	8289	GLUCOSE 1-DEHYDROGENASE II (EC 1.1.1.47)
319	320	RXN01049	VV0079	9633	11114	GLUCONOKINASE (EC 2.7.1.12)
321	322	F RXA01049	GR00296	1502	492	GLUCONOKINASE (EC 2.7.1.12)
323	324	F RXA01050	GR00296	1972	1499	GLUCONOKINASE (EC 2.7.1.12)
325	326	RXA00202	GR00032	1216	275	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR
327	328	RXN00872	VV0127	6557	5604	FRUCTOKINASE (EC 2.7.1.4)
329	330	F RXA00872	GR00240	565	1086	FRUCTOKINASE (EC 2.7.1.4)
331	332	RXN00799	VV0009	58477	56834	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
333	334	F RXA00799	GR00214	1	1584	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
335	336	RXA00032	GR00003	12028	10520	MANNITOL 2-DEHYDROGENASE (EC 1.1.1.67)
337	338	RXA02528	GR00725	6880	7854	FRUCTOSE REPRESSOR
339	340	RXN00316	VV0006	7035	8180	Hypothetical Oxidoreductase (EC 1.1.1.-)
341	342	F RXA00309	GR00053	316	5	GLUCOSE--FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
343	344	RXN00310	VV0006	6616	7050	GLUCOSE--FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
345	346	F RXA00310	GR00053	735	301	GLUCOSE--FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
347	348	RXA00041	GR00007	1246	5	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)
349	350	RXA02026	GR00615	725	6	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)
351	352	RXA02061	GR00626	1842	349	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
353	354	RXN01369	VV0124	595	1776	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
355	356	F RXA01369	GR00398	3	503	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
357	358	F RXA01373	GR00399	595	1302	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
359	360	RXA02611	GR00743	1	1752	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)
361	362	RXA02612	GR00743	1793	3985	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)
363	364	RXN01884	VV0184	1	1890	GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.25) (EC 3.2.1.33)
365	366	F RXA01884	GR00539	3	1475	GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.25) (EC 3.2.1.33)
367	368	RXA01111	GR00306	16981	17427	GLYCOGEN OPERON PROTEIN GLGX (EC 3.2.1.-)
369	370	RXN01550	VV0143	14749	16260	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
371	372	F RXA01550	GR00431	3	1346	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
373	374	RXN02100	VV0318	2	2326	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
375	376	F RXA02100	GR00631	3	920	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
377	378	F RXA02113	GR00633	2	1207	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
379	380	RXA02147	GR00639	15516	16532	ALPHA-AMYLASE (EC 3.2.1.1)
381	382	RXA01478	GR00422	10517	12352	GLUCOAMYLASE G1 AND G2 PRECURSOR (EC 3.2.1.3)
383	384	RXA01888	GR00539	4366	4923	GLUCOSE-RESISTANCE AMYLASE REGULATOR
385	386	RXN01927	VV0127	50623	49244	XYLULOSE KINASE (EC 2.7.1.17)
387	388	F RXA01927	GR00555	3	1118	XYLULOSE KINASE (EC 2.7.1.17)
389	390	RXA02729	GR00762	747	4	RIBOKINASE (EC 2.7.1.15)
391	392	RXA02797	GR00778	1739	2641	RIBOKINASE (EC 2.7.1.15)
393	394	RXA02730	GR00762	1768	731	RIBOSE OPERON REPRESSOR
395	396	RXA02551	GR00729	2193	2552	6-PHOSPHO-BETA-GLUCOSIDASE (EC 3.2.1.86)
397	398	RXA01325	GR00385	5676	5005	DEOXYRIBOSE-PHOSPHATE ALDOLASE (EC 4.1.2.4)
399	400	RXA00195	GR00030	543	1103	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.-)
401	402	RXA00196	GR00030	1094	1708	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.-)
403	404	RXN01562	VV0191	1230	3137	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
405	406	F RXA01562	GR00436	2	1039	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
407	408	F RXA01705	GR00480	971	1573	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
409	410	RXN00879	VV0099	8763	6646	4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25)
411	412	F RXA00879	GR00242	5927	3828	4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25), amylomaltase
413	414	RXN00043	VV0119	3244	2081	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25)
415	416	F RXA00043	GR00007	3244	2081	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25)
417	418	RXN01752	VV0127	35265	33805	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
419	420	F RXA01839	GR00520	1157	510	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
421	422	RXA01859	GR00529	1473	547	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
423	424	RXA00042	GR00007	2037	1279	GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10)
425	426	RXA01482	GR00422	17271	15397	GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2.6.1.16)
427	428	RXN03179	VV0336	2	667	URONATE ISOMERASE (EC 5.3.1.12)
429	430	F RXA02872	GR10013	675	4	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12)
431	432	RXN03180	VV0337	672	163	URONATE ISOMERASE (EC 5.3.1.12)
433	434	F RXA02873	GR10014	672	163	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12)
435	436	RXA02292	GR00662	1611	2285	GALACTOSIDE O-ACETYLTRANSFERASE (EC 2.3.1.18)
437	438	RXA02666	GR00753	7260	6493	D-RIBITOL-5-PHOSPHATE CYTIDYLYLTRANSFERASE (EC 2.7.7.40)
439	440	RXA00202	GR00032	1216	275	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR
441	442	RXA02440	GR00709	5097	4258	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
443	444	RXN01569	VV0009	41086	42444	dTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
445	446	F RXA01569	GR00438	2	427	DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
447	448	F RXA02055	GR00624	7122	8042	DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
449	450	RXA00825	GR00222	222	1154	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
451	452	RXA02054	GR00624	6103	7119	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
453	454	RXN00427	VV0112	7004	6219	dTDP-RHAMNOSYL TRANSFERASE RFBF (EC 2.-.-.-)
455	456	F RXA00427	GR00098	1591	2022	DTDP-RHAMNOSYL TRANSFERASE RFBF (EC 2.-.-.-)
457	458	RXA00327	GR00057	10263	9880	PROTEIN ARAJ
459	460	RXA00328	GR00057	11147	10656	PROTEIN ARAJ
461	462	RXA00329	GR00057	12390	11167	PROTEIN ARAJ
463	464	RXN01554	VV0135	28686	26545	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1 PRECURSOR (EC 3.2.1.39)
465	466	RXN03015	VV0063	289	8	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22)
467	468	RXN03056	VV0028	6258	6935	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.-.-.-)
469	470	RXN03030	VV0009	57006	56443	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
471	472	RXN00401	VV0025	12427	11489	5-DEHYDRO-4-DEOXYGLUCARATE DEHYDRATASE (EC 4.2.1.41)
473	474	RXN02125	VV0102	23242	22442	ALDOSE REDUCTASE (EC 1.1.1.21)
475	476	RXN00200	VV0181	1679	5116	arabinosyl transferase subunit B (EC 2.4.2.-)
477	478	RXN01175	VV0017	39688	38303	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
479	480	RXN01376	VV0091	5610	4750	PUTATIVE GLYCOSYL TRANSFERASE WBIF
481	482	RXN01631	VV0050	47021	46143	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.-.-.-)
483	484	RXN01593	VV0229	13274	12408	NAGD PROTEIN
485	486	RXN00337	VV0197	20369	21418	GALACTOKINASE (EC 2.7.1.6)
487	488	RXS00584	VV0323	5516	6640	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
489	490	RXS02574				BETA-HEXOSAMINIDASE A PRECURSOR (EC 3.2.1.52)
491	492	RXS03215				GLUCOSE--FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
493	494	F RXA01915	GR00549	1	1008	GLUCOSE--FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
495	496	RXS03224				CYCLOMALTODEXTRINASE (EC 3.2.1.54)
497	498	F RXA00038	GR00006	1417	260	CYCLOMALTODEXTRINASE (EC 3.2.1.54)
499	500	RXC00233				protein involved in sugar metabolism
501	502	RXC00236				Membrane Lipoprotein involved in sugar metabolism
503	504	RXC00271				Exported Protein involved in ribose metabolism
505	506	RXC00338				protein involved in sugar metabolism
507	508	RXC00362				Membrane Spanning Protein involved in metabolism of diols
509	510	RXC00412				Amino Acid ABC Transporter ATP-Binding Protein involved in sugar metabolism
511	512	RXC00526				ABC Transporter ATP-Binding Protein involved in sugar metabolism
513	514	RXC01004				Membrane Spanning Protein involved in sugar metabolism
515	516	RXC01017				Cytosolic Protein involved in sugar metabolism
517	518	RXC01021				Cytosolic Kinase involved in metabolism of sugars and thiamin
519	520	RXC01212				ABC Transporter ATP-Binding Protein involved in sugar metabolism
521	522	RXC01306				Membrane Spanning Protein involved in sugar metabolism
523	524	RXC01366				Cytosolic Protein involved in sugar metabolism
525	526	RXC01372				Cytosolic Protein involved in sugar metabolism

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
527	528	RXC01659				protein involved in sugar metabolism
529	530	RXC01663				protein involved in sugar metabolism
531	532	RXC01693				protein involved in sugar metabolism
533	534	RXC01703				Cytosolic Protein involved in sugar metabolism
535	536	RXC02254				Membrane Associated Protein involved in sugar metabolism
537	538	RXC02255				Cytosolic Protein involved in sugar metabolism
539	540	RXC02435				protein involved in sugar metabolism
541	542	F RXA02435	GR00709	825	268	Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
543	544	RXC03216				protein involved in sugar metabolism

TCA-cycle

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
545	546	RXA02175	GR00641	10710	9418	CITRATE SYNTHASE (EC 4.1.3.7)
547	548	RXA02621	GR00746	2647	1829	CITRATE LYASE BETA CHAIN (EC 4.1.3.6)
549	550	RXN00519	VV0144	5585	3372	ISOCITRATE DEHYDROGENASE (NADP) (EC 1.1.1.42)
551	552	F RXA00521	GR00133	2	1060	ISOCITRATE DEHYDROGENASE [NADP] (EC 1.1.1.42)
553	554	RXN02209	VV0304	1	1671	ACONITATE HYDRATASE (EC 4.2.1.3)
555	556	F RXA02209	GR00648	3	1661	ACONITATE HYDRATASE (EC 4.2.1.3)
557	558	RXN02213	VV0305	1378	2151	ACONITATE HYDRATASE (EC 4.2.1.3)
559	560	F RXA02213	GR00649	1330	2046	ACONITATE HYDRATASE (EC 4.2.1.3)
561	562	RXA02056	GR00625	3	2870	2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.2)
563	564	RXA01745	GR00495	2	1495	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
565	566	RXA00782	GR00206	3984	3103	SUCCINYL-COA SYNTHETASE ALPHA CHAIN (EC 6.2.1.5)
567	568	RXA00783	GR00206	5280	4009	SUCCINYL-COA SYNTHETASE BETA CHAIN (EC 6.2.1.5)
569	570	RXN01695	VV0139	11307	12806	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
571	572	F RXA01615	GR00449	8608	9546	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
573	574	F RXA01695	GR00474	4388	4179	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
575	576	RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
577	578	RXN01048	VV0079	12539	11316	MALIC ENZYME (EC 1.1.1.39)
579	580	F RXA01048	GR00296	3	290	MALIC ENZYME (EC 1.1.1.39)
581	582	F RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
583	584	RXN03101	VV0066	2	583	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
585	586	RXN02046	VV0025	15056	14640	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
587	588	RXN00389	VV0025	11481	9922	oxoglutarate semialdehyde dehydrogenase (EC 1.2.1.-)

Table 1 (continued)

Glyoxylate bypass

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
589	590	RXN02399	VV0176	19708	18365	ISOCITRATE LYASE (EC 4.1.3.1)
591	592	F RXA02399	GR00699	478	1773	ISOCITRATE LYASE (EC 4.1.3.1)
593	594	RXN02404	VV0176	20259	22475	MALATE SYNTHASE (EC 4.1.3.2)
595	596	F RXA02404	GR00700	3798	1663	MALATE SYNTHASE (EC 4.1.3.2)
597	598	RXA01089	GR00304	3209	3958	GLYOXYLATE-INDUCED PROTEIN
599	600	RXA01886	GR00539	3203	2430	GLYOXYLATE-INDUCED PROTEIN

Methylcitrate-pathway

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
600	602	RXN03117	VV0092	3087	1576	2-methylisocitrate synthase (EC 5.3.3.-)
601	604	F RXA00406	GR00090	978	4	2-methylisocitrate synthase (EC 5.3.3.-)
603	606	F RXA00514	GR00130	1983	1576	2-methylisocitrate synthase (EC 5.3.3.-)
605	608	RXA00512	GR00130	621	4	2-methylcitrate synthase (EC 4.1.3.31)
607	610	RXA00518	GR00131	3069	2773	2-methylcitrate synthase (EC 4.1.3.31)
609	612	RXA01077	GR00300	4647	6017	2-methylisocitrate synthase (EC 5.3.3.-)
611	614	RXN03144	VV0141	2	901	2-methylisocitrate synthase (EC 5.3.3.-)
613	616	F RXA02322	GR00668	415	5	2-methylisocitrate synthase (EC 5.3.3.-)
615	618	RXA02329	GR00669	607	5	2-methylisocitrate synthase (EC 5.3.3.-)
617	620	RXA02332	GR00671	1906	764	2-methylcitrate synthase (EC 4.1.3.31)
619	622	RXN02333	VV0141	901	1815	methylisocitrate lyase (EC 4.1.3.30)
621	624	F RXA02333	GR00671	2120	1902	methylisocitrate lyase (EC 4.1.3.30)
623	626	RXA00030	GR00003	9590	9979	LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5)

Methyl-Malonyl-CoA-Mutases

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
625	628	RXN00148	VV0167	9849	12059	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
627	630	F RXA00148	GR00023	2002	5	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
629	632	RXA00149	GR00023	3856	2009	METHYLMALONYL-COA MUTASE BETA-SUBUNIT (EC 5.4.99.2)

Table 1 (continued)

Others

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
631	634	RXN00317	VV0197	26879	27532	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
635	636	F RXA00317	GR00055	344	6	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
637	638	RXA02196	GR00645	3956	3264	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
639	640	RXN02461	VV0124	14236	14643	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)

Redox Chain

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
641	642	RXN01744	VV0174	2350	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
643	644	F RXA00055	GR00008	11753	11890	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
645	646	F RXA01744	GR00494	2113	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
647	648	RXA00379	GR00082	212	6	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA
649	650	RXA00385	GR00083	773	435	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA
651	652	RXA01743	GR00494	806	6	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT II (EC 1.10.3.-)
653	654	RXN02480	VV0084	31222	29567	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
655	656	F RXA01919	GR00550	288	4	CYTOCHROME C OXIDASE SUBUNIT I (EC 1.9.3.1)
657	658	F RXA02480	GR00717	1449	601	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
659	660	F RXA02481	GR00717	1945	1334	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
661	662	RXA02140	GR00639	7339	8415	CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1)
663	664	RXA02142	GR00639	9413	10063	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
665	666	RXA02144	GR00639	11025	12248	RIESKE IRON-SULFUR PROTEIN
667	668	RXA02740	GR00763	7613	8542	PROBABLE CYTOCHROME C OXIDASE ASSEMBLY FACTOR
669	670	RXA02743	GR00763	13534	12497	CYTOCHROME AA3 CONTROLLING PROTEIN
671	672	RXA01227	GR00355	1199	1519	FERREDOXIN
673	674	RXA01865	GR00532	436	122	FERREDOXIN
675	676	RXA00680	GR00179	2632	2315	FERREDOXIN VI
677	678	RXA00679	GR00179	2302	1037	FERREDOXIN--NAD(+) REDUCTASE (EC 1.18.1.3)
679	680	RXA00224	GR00032	24965	24015	ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT
681	682	RXA00225	GR00032	25783	24998	ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT
683	684	RXN00606	VV0192	11299	9026	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
685	686	F RXA00606	GR00160	121	1869	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
687	688	RXN00595	VV0192	8642	7113	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
689	690	F RXA00608	GR00160	2253	3017	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
691	692	RXA00913	GR00249	3	2120	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
693	694	RXA00909	GR00247	2552	3406	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
695	696	RXA00700	GR00182	846	43	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2
697	698	RXN00483	VV0086	44824	46287	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
699	700	F RXA00483	GR00119	19106	20569	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3)
701	702	RXA01534	GR00427	1035	547	NADH-DEPENDENT FMN OXYDOREDUCTASE
703	704	RXA00288	GR00046	2646	1636	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
705	706	RXA02741	GR00763	9585	8620	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
707	708	RXN02560	VV0101	9922	10788	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-)
709	710	F RXA02560	GR00731	6339	7160	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-)
711	712	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1)
713	714	RXN03014	VV0058	1273	368	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
715	716	F RXA00910	GR00248	3	1259	Hydrogenase subunits
717	718	RXN01895	VV0117	955	5	NADH DEHYDROGENASE (EC 1.6.99.3)
719	720	F RXA01895	GR00543	2	817	DEHYDROGENASE
721	722	RXA00703	GR00183	2556	271	FORMATE DEHYDROGENASE ALPHA CHAIN (EC 1.2.1.2)
723	724	RXN00705	VV0005	6111	5197	FDHD PROTEIN
725	726	F RXA00705	GR00184	1291	407	FDHD PROTEIN
727	728	RXN00388	VV0025	2081	3091	CYTOCHROME C BIOGENESIS PROTEIN CCSA
729	730	F RXA00388	GR00085	969	667	essential protein similar to cytochrome c
731	732	F RXA00386	GR00084	514	5	RESC PROTEIN, essential protein similar to cytochrome c biogenesis protein
733	734	RXA00945	GR00259	1876	2847	putative cytochrome oxidase
735	736	RXN02556	VV0101	5602	6759	FLAVOHEMOPROTEIN / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)
737	738	F RXA02556	GR00731	2019	3176	FLAVOHEMOPROTEIN
739	740	RXA01392	GR00408	2297	3373	GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18)
741	742	RXA00800	GR00214	2031	3134	GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (EC 1.2.1.1)
743	744	RXA02143	GR00639	10138	11025	QCRC PROTEIN, menaquinol:cytochrome c oxidoreductase
745	746	RXN03096	VV0058	405	4	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
747	748	RXN02036	VV0176	32683	33063	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3)
749	750	RXN02765	VV0317	3552	2794	Hypothetical Oxidorductase
751	752	RXN02206	VV0302	1784	849	Hypothetical Oxidoreductase
753	754	RXN02554	VV0101	4633	4010	Hypothetical Oxidoreductase (EC 1.1.1.-)

ATP-Synthase

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
755	756	RXN01204	VV0121	1270	461	ATP SYNTHASE A CHAIN (EC 3.6.1.34)
757	758	F RXA01204	GR00345	394	1155	ATP SYNTHASE A CHAIN (EC 3.6.1.34)
759	760	RXA01201	GR00344	675	2315	ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34)
761	762	RXN01193	VV0175	5280	3832	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
763	764	F RXA01193	GR00343	15	755	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
765	766	F RXA01203	GR00344	3355	3993	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
767	768	RXN02821	VV0121	324	85	ATP SYNTHASE C CHAIN (EC 3.6.1.34)
769	770	F RXA02821	GR00802	139	318	ATP SYNTHASE C CHAIN (EC 3.6.1.34)
771	772	RXA01200	GR00344	2	610	ATP SYNTHASE DELTA CHAIN (EC 3.6.1.34)
773	774	RXA01194	GR00343	770	1141	ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34)
775	776	RXA01202	GR00344	2375	3349	ATP SYNTHASE GAMMA CHAIN (EC 3.6.1.34)
777	778	RXN02434	VV0090	4923	3274	ATP-BINDING PROTEIN

Cytochrome metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
779	780	RXN00684	VV0005	29864	28581	CYTOCHROME P450 116 (EC 1.14.-.-)
781	782	RXN00387	VV0025	1150	2004	Hypothetical Cytochrome c Biogenesis Protein

TABLE 2 – Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvat corboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," *Biochem. Biophys. Res. Commun.*, 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," *Appl. Microbiol. Biotechnol.*, 51(2):223-228 (1999)
AB018530	dtsR		Kimura, E. et al. "Molecular cloning of a novel gene, dtsR, which rescues the detergent sensitivity of a mutant derived from *Brevibacterium lactofermentum*," *Biosci. Biotechnol. Biochem.*, 60(10):1565-1570 (1996)
AB018531	dtsR1; dtsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamolytransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

AF038651	dciAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," *Microbiology,* 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," *Mol. Cells.,* 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," *Appl. Environ. Microbiol.,* 65(4)1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinate synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.*, 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," *J. Bacteriol.*, 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzmye); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in Corynebacterium glutamicum; Isolation of genes involved in biochemical characterization of corresponding proteins," *FEMS Microbiol.*, 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol aceteyl transferase	
AJ224946	mqo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," *Eur. J. Biochem.*, 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," *Biochemistry*, 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al."Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," *Mol. Microbiol.*, 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," *Microbiology*, 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94

Table 2 (continued)

E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-trypophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)

E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," *J. Bacteriol.*, 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," *FEMS Microbiol. Lett.*, 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," *J. Bacteriol.*, 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," *PNAS USA*, 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," *FEMS Microbiol. Lett.*, 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," *J. Microbiol. Biotechnol.*, 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," *Appl. Environ. Microbiol.*, 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxr	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," *J. Bacteriol.*, 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," *J. Bacteriol.*, 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 56 rRNA sequences," *J. Bacteriol.*, 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene*, 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3'end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene*, 52:191-200 (1987)

Table 2 (continued)

M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," *Gene*, 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.*, 138:1167-1175 (1992)
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.*, 138:1167-1175 (1992)
M89931	aecD; brnQ; yhbw	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbw	Rossol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," *J. Bacteriol.*, 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," *Arch. Microbiol.*, 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," *Appl. Environ. Microbiol.*, 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 tpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; clgIIR	Putative type II 5-cytosoine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," *J. Bacteriol.*, 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," *Gene*, 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?;gamma glutamyl kinase;similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)

Table 2 (continued)

U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of Methylobacillus flagellatum and Corynebacterium glutamicum," *Gene,* 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A Corynebacterium glutamicum gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," *Arch. Microbiol.,* 166(2);76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A Corynebacterium glutamicum gene conferring multidrug resistance in the heterologous host Escherichia coli," *J. Bacteriol.,* 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5''-aminoglycoside phosphotransferase	
U89648		Corynebacterium glutamicum unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the Brevibacterium lactofermentum tryptophan operon," *Nucleic Acids Res.,* 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of Corynebacterium glutamicum and possible mechanisms for modulation of its expression," *Mol. Gen. Genet.,* 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of Corynebacterium glutamicum: Molecular cloning, nucleotide sequence, and expression," *Mol. Gen. Genet.,* 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," *Plant. Mol. Biol.,* 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the Corynebacterium glutamicum fda gene: structural comparison of C. glutamicum fructose-1, 6-biphosphate aldolase to class I and class II aldolases," *Mol. Microbiol.,*
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from Corynebacterium glutamicum," *Nucleic Acids Res.,* 18(21):6421 (1990)
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.,* 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," *Mol. Microbiol.,* 4(11):1819-1830 (1990)

Table 2 (continued)			
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component I	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," *Nucleic Acids Res.*, 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," *Mol. Microbiol.*, 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.*, 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," *Mol. Microbiol.*, 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspertate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," *Mol. Gen. Genet.*, 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomeras," *J. Bacteriol.*, 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," *Mol. Microbiol.*, 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," *Mol. Microbiol.*, 5(12):2995-3005 (1991)
X66078	cop1	Ps1 protein	Joliff, G. et al. "Cloning and nucleotide sequence of the csp1 gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," *Mol. Microbiol.*, 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," *Microbiol.*, 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," *Mol. Microbiol.*, 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," *Mol. Microbiol.*, 14(3):571-581 (1994)

Table 2 (continued)

X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," *Appl. Environ. Microbiol.*, 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," *J. Bacteriol.*, 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," *Biochem. Biophys. Res. Commun.*, 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," *Appl. Microbiol. Biotechnol.*, 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," *J. Bacteriol.*, 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek*, 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek*, 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from Corynebacterium glutamicum," *DNA Seq.*, 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase: sequence analysis," *Microbiology*, 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera Rhodococcus and Norcardia and evidence for the evolutionary origin of the genus Norcardia from within the radiation of Rhodococcus species," *Microbiol.*, 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronemeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of Corynebacterium glutamicum," *J. Bacteriol.*, 177(5):1152-1158 (1995)
X81379	dapE	Succinyldiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of Corynebacterium glutamicum complementing dapE of Escherichia coli," *Microbiology*, 40:3349-56 (1994)

Table 2 (continued)

X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus Corynebacterium deduced from analyses of small-subunit ribosomal DNA sequences," *Int. J. Syst. Bacteriol.*, 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.*, 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.*, 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus Corynebacterium based on 16S rRNA gene sequences," *Int. J. Syst. Bacteriol.*, 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of C. glutamicum proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," *J. Bacteriol.*, 177(20):5991-5993 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," *Microbiology*, 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," *Microbiology*, 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," *J. Bacteriol.*, 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)

Table 2 (continued)

X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from C. glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of Corynebacterium glutamicum," *J. Biol. Chem.*, 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the Corynebacterium glutamicum betP gene, encoding the transport system for the compatible solute glycine betaine," *J. Bacteriol.*, 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of Corynebacterium glutamicum, encoding two enzymes involved in L-lysine synthesis," *Biotechnol. Lett.*, 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from Corynebacterium glutamicum," *Mol. Microbiol.*, 22(5):815-826 (1996)

Table 2 (continued)

X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," *Appl. Environ. Microbiol.*, 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," *Gene*, 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.*, 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," *Nucleic Acids Res.*, 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.*, 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," *Mol. Microbiol.*, 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," *Mol. Gen. Genet.*, 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," *Arch. Microbiol.*, 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," *Microbiology*, 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," *Appl. Microbiol. Biotechnol.*, 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," *Microbiol.*, 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.*, 180(22):6005-6012 (1998)

Table 2 (continued)

Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding glutamine synthetase I," *FEMS Microbiol. Lett.*, 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynephage 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," *Virology*, 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum: Regulation of argS-lysA cluster expression by arginine," *J. Bacteriol.*, 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," *J. Bacteriol.*, 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," *Appl. Environ. Microbiol.*, 60(7)2209-2219 (1994)
Z46753	*16S rDNA*	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.*, 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al "The galE gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmdR gene," *Gene*, 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.*, 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869," *Gene*, 170(1):91-94 (1996)

[1] A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							
Brevibacterium	flavum			B11477					
Brevibacterium	flavum			B11478					
Brevibacterium	flavum	21127							
Brevibacterium	flavum			B11474					
Brevibacterium	healii	15527							
Brevibacterium	ketoglutamicum	21004							
Brevibacterium	ketoglutamicum	21089							
Brevibacterium	ketosoreductum	21914							
Brevibacterium	lactofermentum				70				
Brevibacterium	lactofermentum				74				
Brevibacterium	lactofermentum				77				
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum			B11470					
Brevibacterium	lactofermentum			B11471					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujiokense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japen.

Table 4: Alignment Results

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rxa00013	996	GB_GSS4:AQ713475	581	AQ713475	HS_5402_B2_A12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=978 Col=24 Row=B, genomic survey sequence.	Homo sapiens	37,148	13-Jul-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M.10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M.10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
rxa00014	903	GB_BA1:MTCY3A2	25830	Z83867	Mycobacterium tuberculosis H37Rv complete genome; segment 136/162.	Mycobacterium tuberculosis	58,140	17-Jun-98
		GB_BA1:MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	57,589	8-Aug-97
		GB_BA1:SAPURCLUS	9120	X92429	S.alboniger napH, pur7, pur10, pur6, pur4, pur5 and pur3 genes.	Streptomyces anulatus	55,667	28-Feb-96
rxa00030	513	GB_EST21:C89713	767	C89713	C89713 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSG229, mRNA sequence.	Dictyostelium discoideum	45,283	20-Apr-98
		GB_EST28:AI497294	484	AI497294	fb63g03.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:AFP4_MYOOC P80961 ANTIFREEZE PROTEIN LS-12. ;, mRNA sequence.	Danio rerio	42,991	11-MAR-1999
		GB_EST21:C92167	637	C92167	C92167 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSD179, mRNA sequence.	Dictyostelium discoideum	44,444	12-Jul-99
rxa00032	1632	GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	39,689	12-MAY-1998
		GB_BA2:AF018073	9810	AF018073	Rhodobacter sphaeroides operon regulator (smoC), periplasmic sorbitol-binding protein (smoE), sorbitol/mannitol transport inner membrane protein (smoF), sorbitol/mannitol transport inner membrane protein (smoG), sorbitol/mannitol transport ATP-binding transport protein (smoK), sorbitol dehydrogenase (smoS), mannitol dehydrogenase (mtlK), and periplasmic mannitol-binding protein (smoM) genes, complete cds.	Rhodobacter sphaeroides	48,045	22-OCT-1997
		GB_BA2:AF045245	5930	AF045245	Klebsiella pneumoniae D-arabinitol transporter (dalT), D-arabinitol kinase (dalK), D-arabinitol dehydrogenase (dalD), and repressor (dalR) genes, complete cds.	Klebsiella pneumoniae	38,514	16-Jul-98
rxa00041	1342	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	99,031	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	99,031	07-OCT-1996
		GB_IN1:LMFL5883	31934	AL117384	Leishmania major Friedlin chromosome 23 cosmid L5883, complete sequence.	Leishmania major	43,663	21-OCT-1999
rxa00042	882	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	94,767	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	94,767	07-OCT-1996

Table 4 (continued)

	GB_IN1:CEU33051	4899	U33051	Caenorhabditis elegans sur-2 mRNA, complete cds.	Caenorhabditis elegans	40,276	23-Jan-96
rxa00043 1287	GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	97,591	07-OCT-1996
	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	97,591	08-OCT-1997 (Rel. 52, Created)
	GB_PR3:AC005174	39769	AC005174	Homo sapiens clone UWGC:g1564a012 from 7p14-15, complete sequence.	Homo sapiens	35,879	24-Jun-98
rxa00098 1743	GB_BA1:MSU88433	1928	U88433	Mycobacterium smegmatis phosphoglucose isomerase gene, complete cds.	Mycobacterium smegmatis	62,658	19-Apr-97
	GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	37,638	27-Jul-98
	GB_BA1:MTCY10D7	39800	Z79700	Mycobacterium tuberculosis H37Rv complete genome; segment 44/162.	Mycobacterium tuberculosis	36,784	17-Jun-98
rxa00148 2334	GB_BA1:MTCY277	38300	Z79701	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	Mycobacterium tuberculosis	67,457	17-Jun-98
	GB_BA1:MSGY456	37316	AD000001	Mycobacterium tuberculosis sequence from clone y456.	Mycobacterium tuberculosis	40,883	03-DEC-1996
	GB_BA1:MSGY175	18106	AD000015	Mycobacterium tuberculosis sequence from clone y175.	Mycobacterium tuberculosis	67,457	10-DEC-1996
rxa00149 1971	GB_BA1:MSGY456	37316	AD000001	Mycobacterium tuberculosis sequence from clone y456.	Mycobacterium tuberculosis	35,883	03-DEC-1996
	GB_BA1:MSGY175	18106	AD000015	Mycobacterium tuberculosis sequence from clone y175.	Mycobacterium tuberculosis	51,001	10-DEC-1996
	GB_BA1:MTCY277	38300	Z79701	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	Mycobacterium tuberculosis	51,001	17-Jun-98
rxa00195 684	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	35,735	19-Jun-98
	GB_BA1:MSGB1529CS	36985	L78824	Mycobacterium leprae cosmid B1529 DNA sequence.	Mycobacterium leprae	57,014	15-Jun-96
	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	41,892	19-Jun-98
rxa00196 738	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	41,841	19-Jun-98
	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	36,599	19-Jun-98
	GB_RO:RATCBRQ	10752	M55532	Rat carbohydrate binding receptor gene, complete cds.	Rattus norvegicus	36,212	27-Apr-93
rxa00202 1065	GB_EST11:AA253618	313	AA253618	mw95c10.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:678450 5', mRNA sequence.	Mus musculus	38,816	13-MAR-1997
	GB_EST26:AI390284	490	AI390284	mw96a03.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:678508 5' similar to TR:O09171 O09171 BETAINE-HOMOCYSTEINE METHYLTRANSFERASE;, mRNA sequence.	Mus musculus	42,239	2-Feb-99
	GB_EST26:AI390280	467	AI390280	mw95c10.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:678450 5', mRNA sequence.	Mus musculus	37,307	2-Feb-99
rxa00206 1161	GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	Mycobacterium leprae	58,312	17-Sep-97
	GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	36,632	23-Jun-99

Table 4 (continued)

	GB_BA1:SC6E10	23990	AL109661	Streptomyces coelicolor cosmid 6E10.	Streptomyces coelicolor A3(2)	38,616	5-Aug-99
rxa00224 1074	GB_BA1:BJU32230	1769	U32230	Bradyrhizobium japonicum electron transfer flavoprotein small subunit (etfS) nd large subunit (etfL) genes, complete cds.	Bradyrhizobium japonicum	48,038	25-MAY-1996
	GB_BA1:PDEETFAB	2440	L14864	Paracoccus denitrificans electron transfer flavoprotein alpha and beta subunit genes, complete cds's.	Paracoccus denitrificans	48,351	27-OCT-1993
	GB_HTG3:AC009689	177954	AC009689	Homo sapiens chromosome 4 clone 104_F_7 map 4, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	38,756	28-Aug-99
rxa00225 909	GB_RO:AF060178	2057	AF060178	Mus musculus heparan sulfate 2-sulfotransferase (Hs2st) mRNA, complete cds.	Mus musculus	39,506	18-Jun-98
	GB_GSS11:AQ325043	734	AQ325043	mgxb0020J01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0020J01r, genomic survey sequence.	Magnaporthe grisea	38,333	8-Jan-99
	GB_EST31:AI676413	551	AI676413	etmEST0167 EtH1 Eimeria tenella cDNA clone etmc074 5', mRNA sequence.	Eimeria tenella	35,542	19-MAY-1999
rxa00235 1398	GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	65,759	17-Jun-98
	GB_BA2:AF061753	3721	AF061753	Nitrosomonas europaea CTP synthase (pyrG) gene, partial cds; and enolase (eno) gene, complete cds.	Nitrosomonas europaea	58,941	31-Aug-98
	GB_BA2:AF086791	37867	AF086791	Zymomonas mobilis strain ZM4 clone 67E10 carbamoylphosphate synthetase small subunit (carA), carbamoylphosphate synthetase large subunit (carB), transcription elongation factor (greA), enolase (eno), pyruvate dehydrogenase alpha subunit (pdhA), pyruvate dehydrogenase beta subunit (pdhB), ribonuclease H (rnh), homoserine kinase homolog, alcohol dehydrogenase II (adhB), and excinuclease ABC subunit A (uvrA) genes, complete cds; and unknown genes.	Zymomonas mobilis	61,239	4-Nov-98
rxa00246 1158	GB_BA2:AF012550	2690	AF012550	Acinetobacter sp. BD413 ComP (comP) gene, complete cds.	Acinetobacter sp. BD413	53,726	27-Sep-99
	GB_PAT:E03856	1506	E03856	gDNA encoding alcohol dehydrogenase.	Bacillus stearothermophilus	51,688	29-Sep-97
	GB_BA1:BACADHT	1688	D90421	B.stearothermophilus adhT gene for alcohol dehydrogenase.	Bacillus stearothermophilus	51,602	7-Feb-99
rxa00251 831	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	42,875	17-Jun-98
	GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	40,380	18-Jun-98
	GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	41,789	18-Jun-98
rxa00288 1134	GB_BA2:AF050114	1038	AF050114	Pseudomonas sp. W7 alginate lyase gene, complete cds.	Pseudomonas sp. W7	49,898	03-MAR-1999
	GB_GSS3:B16984	469	B16984	344A14.TVC CIT978SKA1 Homo sapiens genomic clone A-344A14, genomic survey sequence.	Homo sapiens	39,355	4-Jun-98
	GB_IN2:AF144549	7887	AF144549	Aedes albopictus ribosomal protein L34 (rpl34) gene, complete cds.	Aedes albopictus	36,509	3-Jun-99
rxa00293 1035	GB_EST1:T28483	313	T28483	EST46182 Human Kidney Homo sapiens cDNA 3' end similar to flavin-containing monooxygenase 1 (HT:1956), mRNA sequence.	Homo sapiens	42,997	6-Sep-95

Table 4 (continued)

	GB_PR1:HUMFMO1	2134	M64082	Human flavin-containing monooxygenase (FMO1) mRNA, complete cds.	Homo sapiens	37,915	8-Nov-94
	GB_EST32:AI734238	512	AI734238	zb73c05.y5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:309224 5' similar to gb:M64082 DIMETHYLANILINE MONOOXYGENASE (HUMAN);, mRNA sequence.	Homo sapiens	41,502	14-Jun-99
rxa00296 2967	GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 11.H.20 map 12B-12C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 92 unordered pieces.	Drosophila melanogaster	33,890	02-DEC-1999
	GB_EST15:AA531468	414	AA531468	nj63d12.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997175, mRNA sequence.	Homo sapiens	40,821	20-Aug-97
	GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 11.H.20 map 12B-12C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 92 unordered pieces.	Drosophila melanogaster	30,963	02-DEC-1999
rxa00310 558	GB_VI:VMVY16780	186986	Y16780	variola minor virus complete genome.	variola minor virus	35,883	2-Sep-99
	GB_VI:VARCG	186103	L22579	Variola major virus (strain Bangladesh-1975) complete genome.	Variola major virus	34,664	12-Jan-95
	GB_VI:VVCGAA	185578	X69198	Variola virus DNA complete genome.	Variola virus	36,000	13-DEC-1996
rxa00317 777	GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
	GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
	GB_PR3:AC005697	174503	AC005697	Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.	Homo sapiens	36,340	09-OCT-1998
rxa00327 507	GB_BA1:LCATPASEB	1514	X64542	L.casei gene for ATPase beta-subunit.	Lactobacillus casei	34,664	11-DEC-1992
	GB_BA1:LCATPASEB	1514	X64542	L.casei gene for ATPase beta-subunit.	Lactobacillus casei	39,308	11-DEC-1992
rxa00328 615	GB_BA1:STYPUTPE	1887	L01138	Salmonella (S2980) proline permease (putP) gene, 5' end.	Salmonella sp.	39,623	09-MAY-1996
	GB_BA1:STYPUTPF	1887	L01139	Salmonella (S2983) proline permease (putP) gene, 5' end.	Salmonella sp.	39,623	09-MAY-1996
	GB_BA1:STYPUTPI	1889	L01142	Salmonella (S3015) proline permease (putP) gene, 5' end.	Salmonella sp.	42,906	09-MAY-1996
rxa00329 1347	GB_PR3:AC004691	141990	AC004691	Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.	Homo sapiens	38,142	16-MAY-1998
	GB_PR4:AC004916	129014	AC004916	Homo sapiens clone DJ0891L14, complete sequence.	Homo sapiens	38,549	17-Jul-99
	GB_PR3:AC004691	141990	AC004691	Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.	Homo sapiens	35,865	16-MAY-1998
rxa00340 1269	GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	38,940	24-Jun-99
	GB_GSS12:AQ412290	238	AQ412290	RPCI-11-195H2.TV RPCI-11 Homo sapiens genomic clone RPCI-11-195H2, genomic survey sequence.	Homo sapiens	36,555	23-MAR-1999
	GB_PL2:AF112871	2394	AF112871	Astasia longa small subunit ribosomal RNA gene, complete sequence.	Astasia longa	36,465	28-Jun-99
rxa00379 307	GB_HTG1:CEY56A3	224746	AL022280	Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	35,179	6-Sep-99
	GB_HTG1:CEY56A3	224746	AL022280	Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	35,179	6-Sep-99

Table 4 (continued)

	GB_PR2:HS134O19	86897	AL034555	Human DNA sequence from clone 134O19 on chromosome 1p36.11-36.33, complete sequence.	Homo sapiens	40,604	23-Nov-99
rxa00381 729	GB_GSS4:AQ730532	416	AQ730532	HS_2149_A1_C06_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2149 Col=11 Row=E, genomic survey sequence.	Homo sapiens	35,766	15-Jul-99
	GB_EST23:AI120939	561	AI120939	ub74f05.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:M19381 Mouse calmodulin (MOUSE);, mRNA sequence.	Mus musculus	41,113	2-Sep-98
	GB_EST23:AI120939	561	AI120939	ub74f05.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:M19381 Mouse calmodulin (MOUSE);, mRNA sequence.	Mus musculus	41,113	2-Sep-98
rxa00385 362	GB_EST32:AI726450	565	AI726450	BNLGHi5857 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AF015913) Skb1Hs [Homo sapiens], mRNA sequence.	Gossypium hirsutum	41,152	11-Jun-99
	GB_GSS4:AQ740856	768	AQ740856	HS_2274_A2_A07_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2274 Col=14 Row=A, genomic survey sequence.	Homo sapiens	41,360	16-Jul-99
	GB_PR1:HSPAIP	1587	X91809	H.sapiens mRNA for GAIP protein.	Homo sapiens	36,792	29-MAR-1996
rxa00388 1134	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	51,852	17-Jun-98
	GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	51,852	03-DEC-1996
	GB_HTG1:AP000471	72466	AP000471	Homo sapiens chromosome 21 clone B2308H15 map 21q22.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,875	13-Sep-99
rxa00427 909	GB_BA1:MSGY126	37164	AD000012	Mycobacterium tuberculosis sequence from clone y126.	Mycobacterium tuberculosis	60,022	10-DEC-1996
	GB_BA1:MTY13D12	37085	Z80343	Mycobacterium tuberculosis H37Rv complete genome; segment 156/162.	Mycobacterium tuberculosis	60,022	17-Jun-98
	GB_HTG1:CEY48C3	270193	Z92855	Caenorhabditis elegans chromosome II clone Y48C3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	28,013	29-MAY-1999
rxa00483 1587	GB_PR2:HSAF001550	173882	AF001550	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.	Homo sapiens	38,226	22-Aug-97
	GB_BA1:LLCPJW565	12828	Y12736	Lactococcus lactis cremoris plasmid pJW565 DNA, abiiM, abiiR genes and orfX.	Lactococcus lactis subsp. cremoris	37,492	01-MAR-1999
	GB_HTG2:AC006754	206217	AC006754	Caenorhabditis elegans clone Y40B10, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Caenorhabditis elegans	36,648	23-Feb-99
rxa00511 615	GB_PR3:HSE127C11	38423	Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.	Homo sapiens	39,831	23-Nov-99
	GB_PR3:HSE127C11	38423	Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.	Homo sapiens	36,409	23-Nov-99
rxa00512 718	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	56,232	17-Jun-98

Table 4 (continued)

	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	56,143	20-Sep-91
	GB_BA2:ECU73857	128824	U73857	Escherichia coli chromosome minutes 6-8.	Escherichia coli	48,563	14-Jul-99
rxa00517 1164	GB_HTG2:AC006911	298804	AC006911	Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Caenorhabditis elegans	37,889	24-Feb-99
	GB_HTG2:AC006911	298804	AC006911	Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Caenorhabditis elegans	37,889	24-Feb-99
	GB_EST29:AI602158	481	AI602158	UI-R-AB0-vy-a-01-0-UI.s2 UI-R-AB0 Rattus norvegicus cDNA clone UI-R-AB0-vy-a-01-0-UI 3', mRNA sequence.	Rattus norvegicus	40,833	21-Apr-99
rxa00518 320	GB_BA2:ECU73857	128824	U73857	Escherichia coli chromosome minutes 6-8.	Escherichia coli	49,688	14-Jul-99
	GB_BA2:STU51879	8371	U51879	Salmonella typhimurium propionate catabolism operon: RpoN activator protein homolog (prpR), carboxyphosphonoenolpyruvate phosphonomutase homolog (prpB), citrate synthase homolog (prpC), prpD and prpE genes, complete cds.	Salmonella typhimurium	50,313	5-Aug-99
	GB_BA2:AE000140	12498	AE000140	Escherichia coli K-12 MG1655 section 30 of 400 of the complete genome.	Escherichia coli	49,688	12-Nov-98
rxa00606 2378	GB_EST32:AU068253	376	AU068253	AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence.	Oryza sativa	41,333	7-Jun-99
	GB_EST13:AA363046	329	AA363046	EST72922 Ovary II Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	34,347	21-Apr-97
	GB_EST32:AU068253	376	AU068253	AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence.	Oryza sativa	41,899	7-Jun-99
rxa00635 1860	GB_BA1:PAORF1	1440	X13378	Pseudomonas amyloderamosa DNA for ORF 1.	*Pseudomonas amyloderamosa*	*53,912*	*14-Jul-95*
	GB_BA1:PAORF1	1440	X13378	Pseudomonas amyloderamosa DNA for ORF 1.	Pseudomonas amyloderamosa	54,422	14-Jul-95
rxa00679 1389	GB_PL2:AC010871	80381	AC010871	Arabidopsis thaliana chromosome III BAC T16O11 genomic sequence, complete sequence.	Arabidopsis thaliana	38,244	13-Nov-99
	GB_PL1:AT81KBGEN	81493	X98130	A.thaliana 81kb genomic sequence.	Arabidopsis thaliana	36,091	12-MAR-1997
	GB_PL2:AC010871	80381	AC010871	Arabidopsis thaliana chromosome III BAC T16O11 genomic sequence, complete sequence.	Arabidopsis thaliana	37,135	13-Nov-99
rxa00680 441	GB_PR3:AC004058	38400	AC004058	Homo sapiens chromosome 4 clone B241P19 map 4q25, complete sequence.	Homo sapiens	36,165	30-Sep-98
	GB_PL1:AT81KBGEN	81493	X98130	A.thaliana 81kb genomic sequence.	Arabidopsis thaliana	38,732	12-MAR-1997
	GB_PL1:AB026648	43481	AB026648	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence.	Arabidopsis thaliana	38,732	07-MAY-1999
rxa00682 2022	GB_HTG3:AC010325	197110	AC010325	Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces.	Homo sapiens	37,976	15-Sep-99
	GB_HTG3:AC010325	197110	AC010325	Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces.	Homo sapiens	37,976	15-Sep-99
	GB_PR4:AC008179	181745	AC008179	Homo sapiens clone NH0576F01, complete sequence.	Homo sapiens	37,143	28-Sep-99

Table 4 (continued)

rxa00683 1215	GB_BA2:AE000896	10707	AE000896	Methanobacterium thermoautotrophicum from bases 1189349 to 1200055 (section 102 of 148) of the complete genome.	Methanobacterium thermoautotrophicum	38,429	15-Nov-97
	GB_IN1:DMBR7A4	212734	AL109630	Drosophila melanogaster clone BACR7A4.	Drosophila melanogaster	36,454	30-Jul-99
	GB_EST35:AV163010	273	AV163010	AV163010 Mus musculus head C57BL/6J 13-day embryo Mus musculus cDNA clone 3110006J22, mRNA sequence.	Mus musculus	41,758	8-Jul-99
rxa00686 927	GB_HTG2:HSDJ137K2	190223	AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	38,031	03-DEC-1999
	GB_HTG2:HSDJ137K2	190223	AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	38,031	03-DEC-1999
	GB_EST12:AA284399	431	AA284399	zs57b04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701551 5', mRNA sequence.	Homo sapiens	39,205	14-Aug-97
rxa00700 927	GB_EST34:AI785570	454	AI785570	uj44d03.x1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1922789 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN);, mRNA sequence.	Mus musculus	41,943	2-Jul-99
	GB_EST25:AI256147	684	AI256147	ui95e12.x1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1890190 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN);, mRNA sequence.	Mus musculus	40,791	12-Nov-98
	GB_BA1:CARCG12	2079	X14979	C. aurantiacus reaction center genes 1 and 2.	Chloroflexus aurantiacus	37,721	23-Apr-91
rxa00703 2409	GB_BA1:SC7H2	42655	AL109732	Streptomyces coelicolor cosmid 7H2.	Streptomyces coelicolor A3(2)	56,646	2-Aug-99
	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,369	19-Jun-98
	GB_BA2:REU60056	2520	U60056	Ralstonia eutropha formate dehydrogenase-like protein (cbbBc) gene, complete cds.	Ralstonia eutropha	51,087	16-OCT-1996
rxa00705 1038	GB_GSS15:AQ604477	505	AQ604477	HS_2116_B1_G07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2116 Col=13 Row=N, genomic survey sequence.	Homo sapiens	39,617	10-Jun-99
	GB_EST11:AA224340	443	AA224340	zr14e07.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648804 3', mRNA sequence.	Homo sapiens	35,129	11-MAR-1998
	GB_EST5:N30648	291	N30648	yw77b02.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:258219 3', mRNA sequence.	Homo sapiens	43,986	5-Jan-96
rxa00782 1005	GB_BA1:MTCY10D7	39800	Z79700	Mycobacterium tuberculosis H37Rv complete genome; segment 44/162.	Mycobacterium tuberculosis	63,327	17-Jun-98
	GB_BA1:MLCL373	37304	AL035500	Mycobacterium leprae cosmid L373.	Mycobacterium leprae	62,300	27-Aug-99
	GB_BA2:AF128399	2842	AF128399	Pseudomonas aeruginosa succinyl-CoA synthetase beta subunit (sucC) and succinyl-CoA synthetase alpha subunit (sucD) genes, complete cds.	Pseudomonas aeruginosa	53,698	25-MAR-1999
rxa00783 1395	GB_HTG2:AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.	Homo sapiens	35,135	28-Jul-99
	GB_HTG2:AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.	Homo sapiens	35,135	28-Jul-99
	GB_PR3:AC005017	137176	AC005017	Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.	Homo sapiens	35,864	8-Aug-98
rxa00794 1128	GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	40,331	24-Jun-99

Table 4 (continued)

	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	61,170	27-Aug-99
	GB_PR2:HS151B14	128942	Z82188	Human DNA sequence from clone 151B14 on chromosome 22 Contains SOMATOSTATIN RECEPTOR TYPE 3 (SS3R) gene,pseudogene similar to ribosomal protein L39,RAC2 (RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 (P21-RAC2)) gene ESTs, STSs, GSSs and CpG islands, complete sequence.	Homo sapiens	37,455	16-Jun-99
rxa00799 1767	GB_PL2:AF016327	616	AF016327	Hordeum vulgare Barperm1 (perm1) mRNA, partial cds.	Hordeum vulgare	41,311	01-OCT-1997
	GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,845	30-Nov-99
	GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,845	30-Nov-99
rxa00800 1227	GB_BA1:MTV022	13025	AL021925	Mycobacterium tuberculosis H37Rv complete genome; segment 100/162.	Mycobacterium tuberculosis	63,101	17-Jun-98
	GB_BA1:AB019513	4417	AB019513	Streptomyces coelicolor genes for alcohol dehydrogenase and ABC transporter, complete cds.	Streptomyces coelicolor	41,312	13-Nov-98
	GB_PL1:SCSFAARP	7008	X68020	S.cerevisiae SFA and ARP genes.	Saccharomyces cerevisiae	36,288	29-Nov-94
rxa00825 1056	GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	39,980	17-Jun-98
	GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	39,435	27-Aug-99
	GB_BA2:AF169031	1141	AF169031	Xanthomonas oryzae pv. oryzae putative sugar nucleotide epimerase/dehydratase gene, partial cds.	Xanthomonas oryzae pv. oryzae	46,232	14-Sep-99
rxa00871							
rxa00872 1077	GB_IN1:CEF23H12	35564	Z74472	Caenorhabditis elegans cosmid F23H12, complete sequence.	Caenorhabditis elegans	34,502	08-OCT-1999
	GB_HTG2:AC007263	167390	AC007263	Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.	Homo sapiens	35,714	24-MAY-1999
	GB_HTG2:AC007263	167390	AC007263	Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.	Homo sapiens	35,714	24-MAY-1999
rxa00879 2241	GB_BA1:MTV049	40360	AL022021	Mycobacterium tuberculosis H37Rv complete genome; segment 81/162.	Mycobacterium tuberculosis	36,981	19-Jun-98
	GB_PL2:CDU236897	1827	AJ236897	Candida dubliniensis ACT1 gene, exons 1-2.	Candida dubliniensis	38,716	1-Sep-99
	GB_PL1:CAACT1A	3206	X16377	Candida albicans act1 gene for actin.	Candida albicans	36,610	10-Apr-93
rxa00909 955	GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	51,586	12-MAY-1998
	GB_BA1:RMPHA	7888	X93358	Rhizobium meliloti pha[A,B,C,D,E,F,G] genes.	Sinorhizobium meliloti	48,367	12-MAR-1999
	GB_EST16:C23528	317	C23528	C23528 Japanese flounder spleen Paralichthys olivaceus cDNA clone HB5(2), mRNA sequence.	Paralichthys olivaceus	41,640	28-Sep-99
rxa00913 2118	GB_HTG2:AC007734	188267	AC007734	Homo sapiens chromosome 18 clone hRPK.44_O_1 map 18, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces.	Homo sapiens	34,457	5-Jun-99

Table 4 (continued)

		GB_HTG2:AC007734	188267	AC007734	Homo sapiens chromosome 18 clone hRPK.44_O_1 map 18, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces.	Homo sapiens	34,457	5-Jun-99
		GB_EST18:AA709478	406	AA709478	vv34a05.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:1224272 5', mRNA sequence.	Mus musculus	42,065	24-DEC-1997
rxa00945	1095	GB_HTG4:AC010351	220710	AC010351	Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN PROGRESS ***, 68 unordered pieces.	Homo sapiens	36,448	31-OCT-1999
		GB_HTG4:AC010351	220710	AC010351	Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN PROGRESS ***, 68 unordered pieces.	Homo sapiens	36,448	31-OCT-1999
		GB_BA1:MTCY05A6	38631	Z96072	Mycobacterium tuberculosis H37Rv complete genome; segment 120/162.	Mycobacterium tuberculosis	36,218	17-Jun-98
rxa00965								
rxa00999	1575	GB_PAT:E13660	1916	E13660	gDNA encoding 6-phosphogluconate dehydrogenase.	Corynebacterium glutamicum	98,349	24-Jun-98
		GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	38,520	17-Jun-98
		GB_BA1:MLCB1788	39228	AL008609	Mycobacterium leprae cosmid B1788.	Mycobacterium leprae	64,355	27-Aug-99
rxa01015	442	GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	39,860	17-Jun-98
		GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	39,120	17-Jun-98
rxa01025	1119	GB_BA1:SC7A1	32039	AL034447	Streptomyces coelicolor cosmid 7A1.	Streptomyces coelicolor	55,287	15-DEC-1998
		GB_BA1:MSGB1723CS	38477	L78825	Mycobacterium leprae cosmid B1723 DNA sequence.	Mycobacterium leprae	56,847	15-Jun-96
		GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	Mycobacterium leprae	56,676	17-Sep-97
rxa01048	1347	GB_BA2:AF017444	3067	AF017444	Sinorhizobium meliloti NADP-dependent malic enzyme (tme) gene, complete cds.	Sinorhizobium meliloti	53,660	2-Nov-97
		GB_BA1:BSUB0013	218470	Z99116	Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730.	Bacillus subtilis	37,255	26-Nov-97
		GB_VI:HSV2HG52	154746	Z86099	Herpes simplex virus type 2 (strain HG52), complete genome.	human herpesvirus 2	38,081	04-DEC-1998
rxa01049	1605	GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	35,647	2-Sep-97
		GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	35,647	2-Sep-97
		GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	26,180	2-Sep-97
rxa01077	1494	GB_PR3:HSDJ653C5	85237	AL049743	Human DNA sequence from clone 653C5 on chromosome 1p21.3-22.3 Contains CA repeat(D1S435), STSs and GSSs, complete sequence.	Homo sapiens	36,462	23-Nov-99
		GB_BA1:ECU29579	72221	U29579	Escherichia coli K-12 genome; approximately 61 to 62 minutes.	Escherichia coli	41,808	1-Jul-95
		GB_BA1:ECU29579	72221	U29579	Escherichia coli K-12 genome; approximately 61 to 62 minutes.	Escherichia coli	36,130	1-Jul-95
rxa01089	873	GB_GSS8:AQ044021	387	AQ044021	CIT-HSP-2318C18.TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence.	Homo sapiens	36,528	14-Jul-98

Table 4 (continued)

	GB_GSS8:AQ042907	392	AQ042907	CIT-HSP-2318D17.TR CIT-HSP Homo sapiens genomic clone 2318D17, genomic survey sequence.	Homo sapiens	35,969	14-Jul-98
	GB_GSS8:AQ044021	387	AQ044021	CIT-HSP-2318C18.TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence.	Homo sapiens	44,545	14-Jul-98
rxa01093 1554	GB_BA1:CORPYKI	2795	L27126	Corynebacterium pyruvate kinase gene, complete cds.	Corynebacterium glutamicum	100,000	07-DEC-1994
	GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	63,771	17-Jun-98
	GB_BA1:MIU65430	1439	U65430	Mycobacterium intracellulare pyruvate kinase (pykF) gene, complete cds.	Mycobacterium intracellulare	67,061	23-DEC-1996
rxa01099 948	GB_BA2:AF045998	780	AF045998	Corynebacterium glutamicum inositol monophosphate phosphatase (impA) gene, complete cds.	Corynebacterium glutamicum	99,615	19-Feb-98
	GB_BA2:AF051846	738	AF051846	Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4- imidazolecarboxamide isomerase (hisA) gene, complete cds.	Corynebacterium glutamicum	100,000	12-MAR-1998
	GB_GSS1:FR0005503	619	Z89313	F.rubripes GSS sequence, clone 079B16aE8, genomic survey sequence.	Fugu rubripes	37,785	01-MAR-1997
rxa01111 541	GB_PR3:AC004063	177014	AC004063	Homo sapiens chromosome 4 clone B3218, complete sequence.	Homo sapiens	35,835	10-Jul-98
	GB_PR3:HS1178I21	62268	AL109852	Human DNA sequence from clone RP5-1178I21 on chromosome X, complete sequence.	Homo sapiens	37,873	01-DEC-1999
	GB_HTG3:AC009301	163369	AC009301	Homo sapiens clone NH0062F14, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Homo sapiens	37,240	13-Aug-99
rxa01130 687	GB_HTG3:AC009444	164587	AC009444	Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	38,416	22-Aug-99
	GB_HTG3:AC009444	164587	AC009444	Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	38,416	22-Aug-99
	GB_IN1:DMC66A1	34127	AL031227	Drosophila melanogaster cosmid 66A1.	Drosophila melanogaster	38,416	05-OCT-1998
rxa01193 1572	GB_BA1:CGASO19	1452	X76875	C.glutamicum (ASO 19) ATPase beta-subunit gene.	Corynebacterium glutamicum	99,931	27-OCT-1994
	EM_PAT:E09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in	Corynebacterium glutamicum	99,242	07-OCT-1997 (Rel. 52, Created)
	GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	39,153	09-MAR-1995
rxa01194 495	EM_PAT:E09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in	Corynebacterium glutamicum	100,000	07-OCT-1997 (Rel. 52, Created)
	GB_BA1:CGASO19	1452	X76875	C.glutamicum (ASO 19) ATPase beta-subunit gene.	Corynebacterium glutamicum	100,000	27-OCT-1994
	GB_VI:HEPCRE4B	414	X60570	Hepatitis C genomic RNA for putative envelope protein (RE4B isolate).	Hepatitis C virus	36,769	5-Apr-92
rxa01200							

Table 4 (continued)

rxa01201 1764	GB_BA1:SLATPSYNA	8560	Z22606	S.lividans i protein and ATP synthase genes.	Streptomyces lividans	66,269	01-MAY-1995
	GB_BA1:MTCY373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome; segment 57/162.	Mycobacterium tuberculosis	65,437	17-Jun-98
	GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	39,302	09-MAR-1995
rxa01202 1098	GB_BA1:SLATPSYNA	8560	Z22606	S.lividans i protein and ATP synthase genes.	Streptomyces lividans	57,087	01-MAY-1995
	GB_BA1:SLATPSYNA	8560	Z22606	S.lividans i protein and ATP synthase genes.	Streptomyces lividans	38,298	01-MAY-1995
	GB_BA1:MCSQSSHC	5538	Y09978	M.capsulatus orfx, orfy, orfz, sqs and shc genes.	Methylococcus capsulatus	37,626	26-MAY-1998
rxa01204 933	GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	38,395	15-Sep-99
	GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114I16, *** SEQUENCING IN PROGRESS ***, 39 unordered pieces.	Homo sapiens	35,459	04-DEC-1999
	GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114I16, *** SEQUENCING IN PROGRESS ***, 39 unordered pieces.	Homo sapiens	36,117	04-DEC-1999
rxa01216 1124	GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	39,064	17-Jun-98
	GB_BA2:AF017435	4301	AF017435	Methylobacterium extorquens methanol oxidation genes, glmU-like gene, partial cds, and orfL2, orfL1, orfR genes, complete cds.	Methylobacterium extorquens	42,671	10-MAR-1998
	GB_BA1:CCRFLBDBA	4424	M69228	C.crescentus flagellar gene promoter region.	Caulobacter crescentus	41,054	26-Apr-93
rxa01225 1563	GB_BA2:AF058302	25306	AF058302	Streptomyces roseofulvus frenolicin biosynthetic gene cluster, complete sequence.	Streptomyces roseofulvus	36,205	2-Jun-98
	GB_HTG3:AC007301	165741	AC007301	Drosophila melanogaster chromosome 2 clone BACR04B09 (D576) RPCI-98 04.B.9 map 43E12-44F1 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 150 unordered pieces.	Drosophila melanogaster	39,922	17-Aug-99
	GB_HTG3:AC007301	165741	AC007301	Drosophila melanogaster chromosome 2 clone BACR04B09 (D576) RPCI-98 04.B.9 map 43E12-44F1 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 150 unordered pieces.	Drosophila melanogaster	39,922	17-Aug-99
rxa01227 444	GB_BA1:SERFDXA	3869	M61119	Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds.	Saccharopolyspora erythraea	64,908	13-MAR-1996
	GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	62,838	17-Jun-98
	GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	61,712	10-DEC-1996
rxa01242 900	GB_PR3:AC005697	174503	AC005697	Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.	Homo sapiens	35,373	09-OCT-1998
	GB_HTG3:AC010722	160723	AC010722	Homo sapiens clone NH0122L09, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Homo sapiens	39,863	25-Sep-99
	GB_HTG3:AC010722	160723	AC010722	Homo sapiens clone NH0122L09, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Homo sapiens	39,863	25-Sep-99

Table 4 (continued)

rxa01243 1083	GB_GSS10:AQ255057	583	AQ255057	mgxb0008N01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0008N01r, genomic survey sequence.	Magnaporthe grisea	38,722	23-OCT-1998
	GB_IN1:CEK05D4	19000	Z92804	Caenorhabditis elegans cosmid K05D4, complete sequence.	Caenorhabditis elegans	35,448	23-Nov-98
	GB_IN1:CEK05D4	19000	Z92804	Caenorhabditis elegans cosmid K05D4, complete sequence.	Caenorhabditis elegans	35,694	23-Nov-98
rxa01259 981	GB_BA1:CGLPD	1800	Y16642	Corynebacterium glutamicum lpd gene, complete CDS.	Corynebacterium glutamicum	100,000	1-Feb-99
	GB_HTG4:AC010567	143287	AC010567	Drosophila melanogaster chromosome 3L/69C1 clone RPCI98-11N6, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	37,178	16-OCT-1999
	GB_HTG4:AC010567	143287	AC010567	Drosophila melanogaster chromosome 3L/69C1 clone RPCI98-11N6, ***SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	37,178	16-OCT-1999
rxa01262 1284	GB_BA2:AF172324	14263	AF172324	Escherichia coli GalF (galF) gene, partial cds; O-antigen repeat unit transporter Wzx (wzx), WbnA (wbnA), O-antigen polymerase Wzy (wzy), WbnB (wbnB), WbnC (wbnC), WbnD (wbnD), WbnE (wbnE), UDP-Glc-4-epimerase GalE (galE), 6-phosphogluconate dehydrogenase Gnd (gnd), UDP-Glc-6-dehydrogenase Ugd (ugd), and WbnF (wbnF) genes, complete cds; and chain length determinant Wzz (wzz) gene, partial cds.	Escherichia coli	59,719	29-OCT-1999
	GB_BA2:ECU78086	4759	U78086	Escherichia coli hypothetical uridine-5'-diphosphoglucose dehydrogenase (ugd) and O-chain length regulator (wzz) genes, complete cds.	Escherichia coli	59,735	5-Nov-97
	GB_BA1:D90841	20226	D90841	E.coli genomic DNA, Kohara clone #351(45.1-45.5 min.).	Escherichia coli	37,904	21-MAR-1997
rxa01311 870	GB_PR3:AC004103	144368	AC004103	Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.	Homo sapiens	37,340	18-Apr-98
	GB_HTG3:AC007383	215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	36,385	25-Sep-99
	GB_HTG3:AC007383	215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	36,385	25-Sep-99
rxa01312 2142	GB_BA2:AE000487	13889	AE000487	Escherichia coli K-12 MG1655 section 377 of 400 of the complete genome.	Escherichia coli	39,494	12-Nov-98
	GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	46,252	23-Jun-99
	GB_BA1:U00022	36411	U00022	Mycobacterium leprae cosmid L308.	Mycobacterium leprae	46,368	01-MAR-1994
rxa01325 795	GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces.	Homo sapiens	36,016	2-Nov-99
	GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces.	Homo sapiens	36,016	2-Nov-99
	GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces.	Homo sapiens	39,618	2-Nov-99
rxa01332 576	GB_HTG6:AC007186	225851	AC007186	Drosophila melanogaster chromosome 2 clone BACR03D06 (D569) RPCI-98 03.D.6 map 32A-32A strain y; cn bw sp, *** SEQUENCE IN PROGRESS***, 91 unordered pieces.	Drosophila melanogaster	35,366	07-DEC-1999
	GB_HTG6:AC007147	202291	AC007147	Drosophila melanogaster chromosome 2 clone BACR19N18 (D572) RPCI-98 19.N.18 map 32A-32A strain y; cn bw sp, *** SEQUENCE IN PROGRESS ***, 22 unordered pieces.	Drosophila melanogaster	35,366	07-DEC-1999

Table 4 (continued)

	GB_HTG3:AC010207	207890	AC010207	Homo sapiens clone RPCI11-375I20, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.	Homo sapiens	34,821	16-Sep-99
rxa01350 1107	GB_BA2:AF109682	990	AF109682	Aquaspirillum arcticum malate dehydrogenase (MDH) gene, complete cds.	Aquaspirillum arcticum	58,487	19-OCT-1999
	GB_HTG2:AC006759	103725	AC006759	Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS***, 8 unordered pieces.	Caenorhabditis elegans	37,963	25-Feb-99
	GB_HTG2:AC006759	103725	AC006759	Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS***, 8 unordered pieces.	Caenorhabditis elegans	37,963	25-Feb-99
rxa01365 1497	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	38,011	17-Jun-98
	GB_BA1:XANXANAB	3410	M83231	Xanthomonas campestris phosphoglucomutase and phosphomannomutase (xanA) and phosphomannose isomerase and GDP-mannose pyrophosphorylase (xanB) genes, complete cds.	Xanthomonas campestris	47,726	26-Apr-93
	GB_GSS10:AQ194038	697	AQ194038	RPCI11-47D24.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-47D24, genomic survey sequence.	Homo sapiens	36,599	20-Apr-99
rxa01369 1305	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	36,940	17-Jun-98
	GB_GSS3:B10037	974	B10037	T27A19-T7 TAMU Arabidopsis thaliana genomic clone T27A19, genomic survey sequence.	Arabidopsis thaliana	35,284	14-MAY-1997
	GB_GSS3:B09549	1097	B09549	T21A19-T7.1 TAMU Arabidopsis thaliana genomic clone T21A19, genomic survey sequence.	Arabidopsis thaliana	38,324	14-MAY-1997
rxa01377 1209	GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,778	10-Feb-99
	GB_HTG5:AC007547	262181	AC007547	Homo sapiens clone RP11-252O18, WORKING DRAFT SEQUENCE, 121 unordered pieces.	Homo sapiens	32,658	16-Nov-99
	GB_HTG5:AC007547	262181	AC007547	Homo sapiens clone RP11-252O18, WORKING DRAFT SEQUENCE, 121 unordered pieces.	Homo sapiens	38,395	16-Nov-99
rxa01392 1200	GB_BA2:AF072709	8366	AF072709	Streptomyces lividans amplifiable element AUD4: putative transcriptional regulator, putative ferredoxin, putative cytochrome P450 oxidoreductase, and putative oxidoreductase genes, complete cds; and unknown genes.	Streptomyces lividans	55,221	8-Jul-98
	GB_BA1:CGLYSEG	2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	100,000	24-Feb-97
	GB_PR4:AC005906	185952	AC005906	Homo sapiens 12p13.3 BAC RPCI11-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	36,756	30-Jan-99
rxa01436 1314	GB_BA1:CGPTAACKA	3657	X89084	C.glutamicum pta gene and ackA gene.	Corynebacterium glutamicum	100,000	23-MAR-1999
	GB_BA1:D90861	14839	D90861	E.coli genomic DNA, Kohara clone #405(52.0-52.3 min.).	Escherichia coli	53,041	29-MAY-1997
	GB_PAT:E02087	1200	E02087	DNA encoding acetate kinase protein form Escherichia coli.	Escherichia coli	54,461	29-Sep-97
rxa01468 948	GB_GSS1:HPU60627	280	U60627	Helicobacter pylori feoB-like DNA sequence, genomic survey sequence.	Helicobacter pylori	39,286	9-Apr-97
	GB_EST31:AI701691	349	AI701691	we81c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347494 3' similar to gb:L19686_ma1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN);, mRNA sequence.	Homo sapiens	39,412	3-Jun-99

Table 4 (continued)

	GB_EST15:AA480256	389	AA480256	ne31f04.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:898975 3' similar to gb:L19686_rna1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN);, mRNA sequence.	Homo sapiens	39,574	14-Aug-97
rxa01478 1959	GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid I51.	Streptomyces coelicolor A3(2)	54,141	16-Aug-99
	GB_BA1:SCE36	12581	AL049763	Streptomyces coelicolor cosmid E36.	Streptomyces coelicolor	38,126	05-MAY-1999
	GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	41,852	9-Apr-97
rxa01482 1998	GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	62,149	20-Aug-98
	GB_BA1:U00020	36947	U00020	Mycobacterium leprae cosmid B229.	Mycobacterium leprae	38,303	01-MAR-1994
	GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome; segment 146/162.	Mycobacterium tuberculosis	38,179	18-Jun-98
rxa01534							
rxa01535 1530	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	66,208	27-Aug-99
	GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	38,553	24-Jun-99
	GB_BA1:PAU72494	4368	U72494	Pseudomonas aeruginosa fumarase (fumC) and Mn superoxide dismutase (sodA) genes, complete cds.	Pseudomonas aeruginosa	52,690	23-OCT-1996
rxa01550 1635	GB_BA1:D90907	132419	D90907	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885.	Synechocystis sp.	56,487	7-Feb-99
	GB_IN2:AF073177	9534	AF073177	Drosophila melanogaster glycogen phosphorylase (GlyP) gene, complete cds.	Drosophila melanogaster	55,100	1-Jul-99
	GB_IN2:AF073179	3159	AF073179	Drosophila melanogaster glycogen phosphorylase (Glp1) mRNA, complete cds.	Drosophila melanogaster	56,708	27-Apr-99
rxa01562							
rxa01569 1482	GB_BA1:D78182	7836	D78182	Streptococcus mutans DNA for dTDP-rhamnose synthesis pathway, complete cds.	Streptococcus mutans	44,050	5-Feb-99
	GB_BA2:AF079139	4342	AF079139	Streptomyces venezuelae pikCD operon, complete sequence.	Streptomyces venezuelae	38,587	28-OCT-1998
	GB_BA2:AF087022	1470	AF087022	Streptomyces venezuelae cytochrome P450 monooxygenase (picK) gene, complete cds.	Streptomyces venezuelae	38,621	15-OCT-1998
rxa01570 978	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	59,035	17-Jun-98
	GB_BA2:AF097519	4594	AF097519	Klebsiella pneumoniae dTDP-D-glucose 4,6 dehydratase (rmlB), glucose-1-phosphate thymidylyl transferase (rmlA), dTDP-4-keto-L-rhamnose reductase (rmlD), dTDP-4-keto-6-deoxy-D-glucose 3,5-epimerase (rmlC), and rhamnosyl transferase (wbbL) genes, complete cds.	Klebsiella pneumoniae	59,714	4-Nov-98

Table 4 (continued)

	GB_BA2:NGOCPSPS	8905	L09189	Neisseria meningitidis dTDP-D-glucose 4,6-dehydratase (rfbB), glucose-1-phosphate thymidyl transferase (rfbA) and rfbC genes, complete cds and UPD-glucose-4-epimerase (galE) pseudogene.	Neisseria meningitidis	58,384	30-Jul-96
rxa01571 723	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	57,500	7-Aug-98
	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	35,655	7-Aug-98
rxa01572 615	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	57,843	7-Aug-98
	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	38,119	7-Aug-98
rxa01606 2799	GB_VI:CFU72240	4783	U72240	Choristoneura fumiferana nuclear polyhedrosis virus ETM protein homolog, 79 kDa protein homolog, 15 kDa protein homolog and GTA protein homolog genes, complete cds.	Choristoneura fumiferana nucleopolyhedrovirus	37,115	29-Jan-99
	GB_GSS10:AQ213248	408	AQ213248	HS_3249_B1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3249 Col=3 Row=B, genomic survey sequence.	Homo sapiens	34,559	18-Sep-98
	GB_GSS8:AQ070145	285	AQ070145	HS_3027_B1_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=P, genomic survey sequence.	Homo sapiens	40,351	5-Aug-98
rxa01626 468	GB_PR4:AF152510	2490	AF152510	Homo sapiens protocadherin gamma A3 short form protein (PCDH-gamma-A3) variable region sequence, complete cds.	Homo sapiens	34,298	14-Jul-99
	GB_PR4:AF152323	4605	AF152323	Homo sapiens protocadherin gamma A3 (PCDH-gamma-A3) mRNA, complete cds.	Homo sapiens	34,298	22-Jul-99
	GB_PR4:AF152509	2712	AF152509	Homo sapiens PCDH-gamma-A3 gene, aberrantly spliced, mRNA sequence.	Homo sapiens	34,298	14-Jul-99
rxa01632 1128	GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N.2 map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999
	GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N.2 map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999
	GB_GSS8:B99182	415	B99182	CIT-HSP-2280I13.TR CIT-HSP Homo sapiens genomic clone 2280I13, genomic survey sequence.	Homo sapiens	36,111	26-Jun-98
rxa01633 1206	GB_BA1:BSUB0009	208780	Z99112	Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.	Bacillus subtilis	36,591	26-Nov-97
	GB_BA1:BSUB0009	208780	Z99112	Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.	Bacillus subtilis	34,941	26-Nov-97
	GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48I10 (D505) RPCI-98 48.I.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Drosophila melanogaster	37,037	2-Aug-99

Table 4 (continued)

rxa01695 1623	GB_BA1:CGA224946	2408	AJ224946	Corynebacterium glutamicum DNA for L-Malate:quinone oxidoreductase.	Corynebacterium glutamicum	100,000	11-Aug-98
	GB_BA1:MTCY24A1	20270	Z95207	Mycobacterium tuberculosis H37Rv complete genome; segment 124/162.	Mycobacterium tuberculosis	38,626	17-Jun-98
	GB_IN1:DMU15974	2994	U15974	Drosophila melanogaster kinesin-like protein (klp68d) mRNA, complete cds.	Drosophila melanogaster	36,783	18-Jul-95
rxa01702 1155	GB_BA1:CGFDA	3371	X17313	Corynebacterium glutamicum fda gene for fructose-bisphosphate aldolase (EC 4.1.2.13).	Corynebacterium glutamicum	99,913	12-Sep-93
	GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	Mycobacterium tuberculosis	38,786	17-Jun-98
	GB_BA1:MLCB4	36310	AL023514	Mycobacterium leprae cosmid B4.	Mycobacterium leprae	38,238	27-Aug-99
rxa01743 901	GB_IN2:CELC27H5	35840	U14635	Caenorhabditis elegans cosmid C27H5.	Caenorhabditis elegans	35,334	13-Jul-95
	GB_EST24:AI167112	579	AI167112	xylem.est.878 Poplar xylem Lambda ZAPII library Populus balsamifera subsp. trichocarpa cDNA 5', mRNA sequence.	Populus balsamifera subsp. trichocarpa	39,222	03-DEC-1998
	GB_GSS9:AQ102635	347	AQ102635	HS_3048_B1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=15 Row=L, genomic survey sequence.	Homo sapiens	40,653	27-Aug-98
rxa01744 1662	GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	36,650	17-Jun-98
	GB_GSS1:AF009226	665	AF009226	Mycobacterium tuberculosis cytochrome D oxidase subunit I (appC) gene, partial sequence, genomic survey sequence.	Mycobacterium tuberculosis	63,438	31-Jul-97
	GB_BA1:SCD78	36224	AL034355	Streptomyces coelicolor cosmid D78.	Streptomyces coelicolor	53,088	26-Nov-98
rxa01745 836	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	62,081	17-Jun-98
	GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	61,364	22-Aug-97
	GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	52,323	12-Nov-98
rxa01758 1140	GB_PR3:HS57G9	113872	Z95116	Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.	Homo sapiens	39,209	23-Nov-99
	GB_PL2:YSCH9666	39057	U10397	Saccharomyces cerevisiae chromosome VIII cosmid 9666.	Saccharomyces cerevisiae	40,021	5-Sep-97
	GB_PL2:YSCH9986	41664	U00027	Saccharomyces cerevisiae chromosome VIII cosmid 9986.	Saccharomyces cerevisiae	34,375	29-Aug-97
rxa01814 1785	GB_BA1:ABCCELB	2058	L24077	Acetobacter xylinum phosphoglucomutase (celB) gene, complete cds.	Acetobacter xylinus	62,173	21-Sep-94
	GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	39,749	17-Jun-98
	GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	40,034	17-Jun-98
rxa01851 1809	GB_GSS9:AQ142579	529	AQ142579	HS_2222_B1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=5 Row=P, genomic survey sequence.	Homo sapiens	38,068	24-Sep-98
	GB_IN2:AC005889	108924	AC005889	Drosophila melanogaster, chromosome 2L, region 30A3- 30A6, P1 clones DS06958 and DS03097, complete sequence.	Drosophila melanogaster	36,557	30-OCT-1998
	GB_GSS1:AG008814	637	AG008814	Homo sapiens genomic DNA, 21q region, clone: B137B7BB68, genomic survey sequence.	Homo sapiens	35,316	7-Feb-99

Table 4 (continued)

rxa01859 1050	GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,364	03-OCT-1999
	GB_HTG5:AC008031	158889	AC008031	Trypanosoma brucei chromosome II clone RPCI93-25N14, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Trypanosoma brucei	35,334	15-Nov-99
	GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,529	03-OCT-1999
rxa01865 438	GB_BA1:SERFDXA	3869	M61119	Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds.	Saccharopolyspora erythraea	59,862	13-MAR-1996
	GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	61,949	17-Jun-98
	GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	59,908	10-DEC-1996
rxa01882 1113	GB_PR1:HUMADRA2C	1491	J03853	Human kidney alpha-2-adrenergic receptor mRNA, complete cds.	Homo sapiens	36,899	27-Apr-93
	GB_PR4:HSU72648	4850	U72648	Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.	Homo sapiens	36,899	23-Nov-98
	GB_GSS3:B42200	387	B42200	HS-1055-B1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 777 Col=5 Row=B, genomic survey sequence.	Homo sapiens	34,805	18-OCT-1997
rxa01884 1913	GB_BA1:MTCY48	35377	Z74020	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162.	Mycobacterium tuberculosis	37,892	17-Jun-98
	GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	40,413	29-MAR-1999
	GB_BA1:D90908	122349	D90908	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234.	Synechocystis sp.	47,792	7-Feb-99
rxa01886 897	GB_GSS9:AQ116291	572	AQ116291	RPCI11-49P6.TK.1 RPCI-11 Homo sapiens genomic clone RPCI-11-49P6, genomic survey sequence.	Homo sapiens	43,231	20-Apr-99
	GB_BA2:AE001721	17632	AE001721	Thermotoga maritima section 33 of 136 of the complete genome.	Thermotoga maritima	39,306	2-Jun-99
	GB_EST16:AA567090	596	AA567090	GM01044.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM01044 5prime, mRNA sequence.	Drosophila melanogaster	42,807	28-Nov-98
rxa01887 1134	GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***, 102 unordered pieces.	Homo sapiens	36,417	03-DEC-1999
	GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***, 102 unordered pieces.	Homo sapiens	37,667	03-DEC-1999
	GB_BA2:ALW243431	26953	AJ243431	Acinetobacter lwoffii wzc, wzb, wza, weeA, weeB, wceC, wzx, wzy, weeD, weeE, weeF, weeG, weeH, weeI, weeJ, weeK, galU, ugd, pgi, galE, pgm (partial) and mip (partial) genes (emulsan biosynthetic gene cluster), strain RAG-1.	Acinetobacter lwoffii	39,640	01-OCT-1999
rxa01888 658	GB_HTG2:AC008197	125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPCI-98 02.L.12 map 94B-94C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 113 unordered pieces.	Drosophila melanogaster	32,969	2-Aug-99

Table 4 (continued)

	GB_HTG2:AC008197	125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPCI-98 02.L.12 map 94B-94C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 113 unordered pieces.	Drosophila melanogaster	32,969	2-Aug-99
	GB_EST36:AI881527	598	AI881527	606070C09.y1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, mRNA sequence.	Zea mays	43,617	21-Jul-99
rxa01891 887	GB_VI:HIV232971	621	AJ232971	Human immunodeficiency virus type 1 subtype C nef gene, patient MP83.	Human immunodeficiency virus type 1	40,040	05-MAR-1999
	GB_PL1:AFCHSE	6158	Y09542	A.fumigatus chsE gene.	Aspergillus fumigatus	37,844	1-Apr-97
	GB_PR3:AF064858	193387	AF064858	Homo sapiens chromosome 21q22.3 BAC 28F9, complete sequence.	Homo sapiens	37,136	2-Jun-98
rxa01895 1051	GB_BA1:CGL238250	1593	AJ238250	Corynebacterium glutamicum ndh gene.	Corynebacterium glutamicum	100,000	24-Apr-99
	GB_BA2:AF038423	1376	AF038423	Mycobacterium smegmatis NADH dehydrogenase (ndh) gene, complete cds.	Mycobacterium smegmatis	65,254	05-MAY-1998
	GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	40,058	17-Jun-98
rxa01901 1383	GB_BA1:MSGB38COS	37114	L01095	M. leprae genomic DNA sequence, cosmid B38 bfr gene, complete cds.	Mycobacterium leprae	59,551	6-Sep-94
	GB_BA1:SCE63	37200	AL035640	Streptomyces coelicolor cosmid E63.	Streptomyces coelicolor	39,468	17-MAR-1999
	GB_PR3:AF093117	147216	AF093117	Homo sapiens chromosome 7qtelo BAC E3, complete sequence.	Homo sapiens	39,291	02-OCT-1998
rxa01927 1503	GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	38,384	11-MAY-1999
	GB_BA1:ASXYLA	1905	X59466	Arthrobacter Sp. N.R.R.L. B3728 xylA gene for D-xylose(D-glucose) isomerase.	Arthrobacter sp.	56,283	04-MAY-1992
	GB_HTG3:AC009500	176060	AC009500	Homo sapiens clone NH0511A20, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces.	Homo sapiens	37,593	24-Aug-99
rxa01952 1836	GB_BA2:AE000739	13335	AE000739	Aquifex aeolicus section 71 of 109 of the complete genome.	Aquifex aeolicus	36,309	25-MAR-1998
	GB_EST28:AI519629	612	AI519629	LD39282.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD39282 5prime, mRNA sequence.	Drosophila melanogaster	41,941	16-MAR-1999
	GB_EST21:AA949396	767	AA949396	LD28277.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD28277 5prime, mRNA sequence.	Drosophila melanogaster	39,855	25-Nov-98
rxa01989 630	GB_BA1:BSPGIA	1822	X16639	Bacillus stearothermophilus pgiA gene for phosphoglucoisomerase isoenzyme A (EC 5.3.1.9).	Bacillus stearothermophilus	66,292	20-Apr-95
	GB_BA1:BSUB0017	217420	Z99120	Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.	Bacillus subtilis	37,255	26-Nov-97
	GB_BA2:AF132127	8452	AF132127	Streptococcus mutans sorbitol phosphoenolpyruvate:sugar phosphotransferase operon, complete sequence and unknown gene.	Streptococcus mutans	63,607	28-Sep-99
rxa02026 720	GB_BA1:SXSCRBA	3161	X67744	S.xylosus scrB and scrR genes.	Staphylococcus xylosus	67,778	28-Nov-96
	GB_BA1:BSUB0020	212150	Z99123	Bacillus subtilis complete genome (section 20 of 21): from 3798401 to 4010550.	Bacillus subtilis	35,574	26-Nov-97
	GB_BA1:BSGENR	97015	X73124	B.subtilis genomic region (325 to 333).	Bacillus subtilis	51,826	2-Nov-93
rxa02028 526	GB_BA1:MTCI237	27030	Z94752	Mycobacterium tuberculosis H37Rv complete genome; segment 46/162.	Mycobacterium tuberculosis	54,476	17-Jun-98

Table 4 (continued)

	GB_PL2:SCE9537	66030	U18778	Saccharomyces cerevisiae chromosome V cosmids 9537, 9581, 9495, 9867, and lambda clone 5898.	Saccharomyces cerevisiae	36,100	1-Aug-97
	GB_GSS13:AQ501177	767	AQ501177	V26G9 mTn-3xHA/lacZ Insertion Library Saccharomyces cerevisiae genomic 5', genomic survey sequence.	Saccharomyces cerevisiae	32,039	29-Apr-99
rxa02054 1140	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	61,896	27-Aug-99
	GB_BA1:MTY13E12	43401	Z95390	Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.	Mycobacterium tuberculosis	59,964	17-Jun-98
	GB_BA1:MTU43540	3453	U43540	Mycobacterium tuberculosis rfbA, rhamnose biosynthesis protein (rfbA), and rmlC genes, complete cds.	Mycobacterium tuberculosis	59,659	14-Aug-97
rxa02056 2891	GB_PAT:E14601	4394	E14601	Brevibacterium lactofermentum gene for alpha-ketoglutaric acid dehydrogenase.	Corynebacterium glutamicum	98,928	28-Jul-99
	GB_BA1:D84102	4394	D84102	Corynebacterium glutamicum DNA for 2-oxoglutarate dehydrogenase, complete cds.	Corynebacterium glutamicum	98,928	6-Feb-99
	GB_BA1:MTV006	22440	AL021006	Mycobacterium tuberculosis H37Rv complete genome; segment 54/162.	Mycobacterium tuberculosis	39,265	18-Jun-98
rxa02061 1617	GB_HTG7:AC005883	211682	AC005883	Homo sapiens chromosome 17 clone RP11-958E11 map 17, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	37,453	08-DEC-1999
	GB_PL2:ATAC003033	84254	AC003033	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711	19-DEC-1997
	GB_PL2:ATAC002334	75050	AC002334	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711	04-MAR-1998
rxa02063 1350	GB_BA1:SCGLGC	1518	X89733	S.coelicolor DNA for glgC gene.	Streptomyces coelicolor	56,972	12-Jul-99
	GB_GSS4:AQ687350	786	AQ687350	nbxb0074H11r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0074H11r, genomic survey sequence.	Oryza sativa	40,696	1-Jul-99
	GB_EST38:AW028530	444	AW028530	wv27f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2530795 3' similar to WP:T03G11.6 CE04874 ;, mRNA sequence.	Homo sapiens	36,795	27-OCT-1999
rxa02100 2348	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	40,156	10-DEC-1996
	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	55,218	17-Jun-98
	GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism clusterI.	Streptomyces coelicolor	38,475	29-MAR-1999
rxa02122 822	GB_BA1:D90858	13548	D90858	E.coli genomic DNA, Kohara clone #401(51.3-51.6 min.).	Escherichia coli	38,586	29-MAY-1997
	GB_EST37:AI948595	469	AI948595	wq07d12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2470583 3', mRNA sequence.	Homo sapiens	37,259	6-Sep-99
	GB_HTG3:AC010387	220665	AC010387	Homo sapiens chromosome 5 clone CITB-H1_2074D8, *** SEQUENCING IN PROGRESS ***, 77 unordered pieces.	Homo sapiens	38,868	15-Sep-99
rxa02140 1200	GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	51,399	15-Jun-96
	GB_BA1:MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	51,399	15-Jun-96
	GB_RO:AF093099	2482	AF093099	Mus musculus transcription factor TBLYM (Tblym) mRNA, complete cds.	Mus musculus	36,683	01-OCT-1999
rxa02142 774	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	57,292	17-Jun-98

Table 4 (continued)

	GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	35,058	24-MAR-1999
	GB_BA1:AB016787	5550	AB016787	Pseudomonas putida genes for cytochrome o ubiquinol oxidase A-E and 2 ORFs, complete cds.	Pseudomonas putida	47,403	5-Aug-99
rxa02143 1011	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	57,317	17-Jun-98
	GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	38,159	15-Jun-96
	GB_BA1:MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	38,159	15-Jun-96
rxa02144 1347	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	55,530	17-Jun-98
	GB_HTG3:AC011500_0	300851	AC011500	Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS ***, 246 unordered pieces.	Homo sapiens	39,659	18-Feb-00
	GB_HTG3:AC011500_0	300851	AC011500	Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS ***, 246 unordered pieces.	Homo sapiens	39,659	18-Feb-00
rxa02147 1140	GB_EST28:AI492095	485	AI492095	tg07a01.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108040 3', mRNA sequence.	Homo sapiens	39,798	30-MAR-1999
	GB_EST10:AA157467	376	AA157467	zo50e01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence.	Homo sapiens	36,436	11-DEC-1996
	GB_EST10:AA157467	376	AA157467	zo50e01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence.	Homo sapiens	36,436	11-DEC-1996
rxa02149 1092	GB_PR3:HSBK277P6	61698	AL117347	Human DNA sequence from clone 277P6 on chromosome 1q25.3-31.2, complete sequence.	Homo sapiens	36,872	23-Nov-99
	GB_BA2:EMB065R075	360	AF116423	Rhizobium etli mutant MB045 RosR-transcriptionally regulated sequence.	Rhizobium etli	43,175	06-DEC-1999
	GB_EST34:AI789323	574	AI789323	uk53g05.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1972760 5' similar to WP:K11H12.8 CE12160 ;, mRNA sequence.	Mus musculus	39,715	2-Jul-99
rxa02175 1416	GB_BA1:CGGLTG	3013	X66112	C.glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	100,000	17-Feb-95
	GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.	Mycobacterium tuberculosis	64,331	17-Jun-98
	GB_BA1:MLCB57	38029	Z99494	Mycobacterium leprae cosmid B57.	Mycobacterium leprae	62,491	10-Feb-99
rxa02196 816	GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds.	Rattus norvegicus	38,791	31-MAY-1995
	GB_GSS8:AQ012162	763	AQ012162	127PB037070197 Cosmid library of chromosome II Rhodobacter sphaeroides genomic clone 127PB037070197, genomic survey sequence.	Rhodobacter sphaeroides	40,044	4-Jun-98
	GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds.	Rattus norvegicus	37,312	31-MAY-1995
rxa02209 1694	GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	99,173	3-Apr-99
	GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	40,219	26-MAR-1998

Table 4 (continued)

	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	38,253	17-Jun-98
rxa02213 874	GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	99,096	3-Apr-99
	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	34,937	17-Jun-98
	GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	36,885	26-MAR-1998
rxa02245 780	GB_BA2:RCU23145	5960	U23145	Rhodobacter capsulatus Calvin cycle carbon dioxide fixation operon: fructose-1,6-/sedoheptulose-1,7-bisphosphate aldolase (cbbA) gene, partial cds, Form II ribulose-1,5-bisphosphate carboxylase/oxygenase (cbbM) gene, complete cds, and Calvin cycle operon: pentose-5-phosphate-3-epimerase (cbbE), phosphoglycolate phosphatase (cbbZ), and cbbY genes, complete cds.	Rhodobacter capsulatus	48,701	28-OCT-1997
	GB_BA1:ECU82664	139818	U82664	Escherichia coli minutes 9 to 11 genomic sequence.	Escherichia coli	39,119	11-Jan-97
	GB_HTG2:AC007922	158858	AC007922	Homo sapiens chromosome 18 clone hRPK.178_F_10 map 18, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	33,118	26-Jun-99
rxa02256 1125	GB_BA1:CGGAPPGK	3804	X59403	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	99,289	05-OCT-1992
	GB_BA1:SCC54	30753	AL035591	Streptomyces coelicolor cosmid C54.	Streptomyces coelicolor	36,951	11-Jun-99
	GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	64,196	19-Jun-98
rxa02257 1338	GB_BA1:CGGAPPGK	3804	X59403	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	98,873	05-OCT-1992
	GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	61,273	19-Jun-98
	GB_BA2:MAU82749	2530	U82749	Mycobacterium avium glyceraldehyde-3-phosphate dehydrogenase homolog (gapdh) gene, complete cds; and phosphoglycerate kinase gene, partial cds.	Mycobacterium avium	61,772	6-Jan-98
rxa02258 900	GB_BA1:CGGAPPGK	3804	X59403	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	99,667	05-OCT-1992
	GB_BA1:CORPEPC	4885	M25819	C.glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
	GB_PAT:A09073	4885	A09073	C.glutamicum ppg gene for phosphoenol pyruvate carboxylase.	Corynebacterium glutamicum	100,000	25-Aug-93
rxa02259 2895	GB_BA1:CORPEPC	4885	M25819	C.glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
	GB_PAT:A09073	4885	A09073	C.glutamicum ppg gene for phosphoenol pyruvate carboxylase.	Corynebacterium glutamicum	100,000	25-Aug-93
	GB_BA1:CGPPC	3292	X14234	Corynebacterium glutamicum phosphoenolpyruvate carboxylase gene (EC 4.1.1.31).	Corynebacterium glutamicum	99,827	12-Sep-93

Table 4 (continued)

rxa02288 969	GB_PR3:HSDJ94E24	243145	AL050317	Human DNA sequence from clone RP1-94E24 on chromosome 20q12, complete sequence.	Homo sapiens	36,039	03-DEC-1999
	GB_HTG3:AC010091	159526	AC010091	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	35,331	11-Sep-99
	GB_HTG3:AC010091	159526	AC010091	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	35,331	11-Sep-99
rxa02292 798	GB_BA2:AF125164	26443	AF125164	Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.	Bacteroides fragilis	39,747	01-DEC-1999
	GB_GSS5:AQ744695	827	AQ744695	HS_5505_A2_C06_SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=12 Row=E, genomic survey sequence.	Homo sapiens	39,185	16-Jul-99
	GB_EST14:AA381925	309	AA381925	EST95058 Activated T-cells I Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	35,922	21-Apr-97
rxa02322 511	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	57,677	17-Jun-98
	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	37,143	17-Jun-98
rxa02326 939	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	100,000	08-MAY-1998
	GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	100,000	24-DEC-1997
	GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	37,363	17-Jun-98
rxa02327 1083	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	99,259	08-MAY-1998
	GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	99,259	24-DEC-1997
	GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	41,317	17-Jun-98
rxa02328 1719	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	100,000	08-MAY-1998
	GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	100,000	24-DEC-1997
	GB_PL2:AF097728	3916	AF097728	Aspergillus terreus pyruvate carboxylase (Pyc) mRNA, complete cds.	Aspergillus terreus	52,248	29-OCT-1998
rxa02332 1266	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,460	20-Sep-91
	GB_BA2:ABU85944	1334	U85944	Antarctic bacterium DS2-3R citrate synthase (cisy) gene, complete cds.	Antarctic bacterium DS2-3R	57,154	23-Sep-97
	GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	38,164	12-Nov-98
rxa02333 1038	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,929	20-Sep-91
	GB_PR4:HUAC002299	171681	AC002299	Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 ~complete genomic sequence, complete sequence.	Homo sapiens	33,070	23-Nov-99

Table 4 (continued)

	GB_HTG2:AC007889	127840	AC007889	Drosophila melanogaster chromosome 3 clone BACR48E12 (D695) RPCI-98 48.E.12 map 87A-87B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 86 unordered pieces.	Drosophila melanogaster	34,897	2-Aug-99
rxa02399 1467	GB_BA1:CGACEA	2427	X75504	C.glutamicum aceA gene and thiX genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
	GB_BA1:CORACEA	1905	L28760	Corynebacterium glutamicum isocitrate lyase (aceA) gene.	Corynebacterium glutamicum	100,000	10-Feb-95
	GB_PAT:I13693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	99,795	26-Sep-95
rxa02404 2340	GB_BA1:CGACEB	3024	X78491	C.glutamicum (ATCC 13032) aceB gene.	Corynebacterium glutamicum	99,914	13-Jan-95
	GB_BA1:CORACEB	2725	L27123	Corynebacterium glutamicum malate synthase (aceB) gene, complete cds.	Corynebacterium glutamicum	99,786	8-Jun-95
	GB_BA1:PFFC2	5588	Y11998	P.fluorescens FC2.1, FC2.2, FC2.3c, FC2.4 and FC2.5c open reading frames.	Pseudomonas fluorescens	63,539	11-Jul-97
rxa02414 870	GB_PR4:AC007102	176258	AC007102	Homo sapiens chromosome 4 clone C0162P16 map 4p16, complete sequence.	Homo sapiens	35,069	2-Jun-99
	GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,885	03-OCT-1999
	GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,885	03-OCT-1999
rxa02435 681	GB_BA2:AF101055	7457	AF101055	Clostridium acetobutylicum atp operon, complete sequence.	Clostridium acetobutylicum	39,605	03-MAR-1999
	GB_OM:RABPKA	4441	J03247	Rabbit phosphorylase kinase (alpha subunit) mRNA, complete cds.	Oryctolagus cuniculus	36,061	27-Apr-93
	GB_OM:RABPLASISM	4458	M64656	Oryctolagus cuniculus phosphorylase kinase alpha subunit mRNA, complete cds.	Oryctolagus cuniculus	36,000	22-Jun-98
rxa02440 963	GB_EST14:AA417723	374	AA417723	zv01b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746207 3' similar to contains Alu repetitive element;contains element L1 repetitive element ;, mRNA sequence.	Homo sapiens	38,770	16-OCT-1997
	GB_EST11:AA215428	303	AA215428	zr95a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683412 3' similar to contains Alu repetitive element;, mRNA sequence.	Homo sapiens	39,934	13-Aug-97
	GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome; segment 146/162.	Mycobacterium tuberculosis	38,889	18-Jun-98
rxa02453 876	GB_EST14:AA426336	375	AA426336	zv53g02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757394 3', mRNA sequence.	Homo sapiens	38,043	16-OCT-1997
	GB_BA1:STMAACC8	1353	M55426	S.fradiae aminoglycoside acetyltransferase (aacC8) gene, complete cds.	Streptomyces fradiae	37,097	05-MAY-1993
	GB_PR3:AC004500	77538	AC004500	Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.	Homo sapiens	33,256	30-MAR-1998
rxa02474 897	GB_BA1:AB009078	2686	AB009078	Brevibacterium saccharolyticum gene for L-2.3-butanediol dehydrogenase, complete cds.	Brevibacterium saccharolyticum	96,990	13-Feb-99
	GB_OM:BTU71200	877	U71200	Bos taurus acetoin reductase mRNA, complete cds.	Bos taurus	51,659	8-Oct-97
	GB_EST2:F12685	287	F12685	HSC3DA031 normalized infant brain cDNA Homo sapiens cDNA clone c-3da03, mRNA sequence	Homo sapiens	41,509	14-Mar-95
rxa02480 1779	GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	36,737	23-Jun-99

Table 4 (continued)

	GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	35,511	24-MAR-1999
rxa02485	GB_BA1:AP000060	347800	AP000060	Aeropyrum pernix genomic DNA, section 3/7.	Aeropyrum pernix	48,014	22-Jun-99
rxa02492 840	GB_BA1:STMPGM	921	M83661	Streptomyces coelicolor phosphoglycerate mutase (PGM) gene, complete cds.	Streptomyces coelicolor	65,672	26-Apr-93
	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	61,436	17-Jun-98
	GB_BA1:U00018	42991	U00018	Mycobacterium leprae cosmid B2168.	Mycobacterium leprae	37,893	01-MAR-1994
rxa02528 1098	GB_PR2:HS161N10	56075	AL008707	Human DNA sequence from PAC 161N10 on chromosome Xq25. Contains EST.	Homo sapiens	37,051	23-Nov-99
	GB_HTG2:AC008235	136017	AC008235	Drosophila melanogaster chromosome 3 clone BACR15B19 (D995) RPCI-98 15.B.19 map 94F-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 125 unordered pieces.	Drosophila melanogaster	36,822	2-Aug-99
	GB_HTG2:AC008235	136017	AC008235	Drosophila melanogaster chromosome 3 clone BACR15B19 (D995) RPCI-98 15.B.19 map 94F-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 125 unordered pieces.	Drosophila melanogaster	36,822	2-Aug-99
rxa02539 1641	GB_BA2:RSU17129	17425	U17129	Rhodococcus erythropolis ThcA (thcA) gene, complete cds; and unknown genes.	Rhodococcus erythropolis	66,117	16-Jul-99
	GB_BA1:MTV038	16094	AL021933	Mycobacterium tuberculosis H37Rv complete genome; segment 24/162.	Mycobacterium tuberculosis	65,174	17-Jun-98
	GB_BA2:AF068264	3152	AF068264	Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA)gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinoline quinone synthesis A (pqqA) genes, complete cds; and pyrroloquinoline quinone synthesis B (pqqB) gene, partial cds.	Pseudomonas aeruginosa	65,448	18-MAR-1999
rxa02551 483	GB_BA1:BACHYPTP	17057	D29985	Bacillus subtilis wapA and orf genes for wall-associated protein and hypothetical proteins.	Bacillus subtilis	53,602	7-Feb-99
	GB_BA1:BACHUTWAP	28954	D31856	Bacillus subtilis genome containing the hut and wapA loci.	Bacillus subtilis	53,602	7-Feb-99
	GB_BA1:BSGBGLUC	4290	Z34526	B.subtilis (Marburg 168) genes for beta-glucoside permease and beta-glucosidase.	Bacillus subtilis	53,602	3-Jul-95
rxa02556 1281	GB_HTG3:AC008128	335761	AC008128	Homo sapiens, *** SEQUENCING IN PROGRESS ***, 106 unordered pieces.	Homo sapiens	34,022	22-Aug-99
	GB_HTG3:AC008128	335761	AC008128	Homo sapiens, *** SEQUENCING IN PROGRESS ***, 106 unordered pieces.	Homo sapiens	34,022	22-Aug-99
	GB_PL2:AC005292	99053	AC005292	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence.	Arabidopsis thaliana	33,858	16-Apr-99
rxa02560 990	GB_IN1:CEF07A11	35692	Z66511	Caenorhabditis elegans cosmid F07A11, complete sequence.	Caenorhabditis elegans	36,420	2-Sep-99
	GB_EST32:AI731605	566	AI731605	BNLGHi10201 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004684) hypothetical protein [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	38,095	11-Jun-99
	GB_IN1:CEF07A11	35692	Z66511	Caenorhabditis elegans cosmid F07A11, complete sequence.	Caenorhabditis elegans	33,707	2-Sep-99

Table 4 (continued)

rxa02572 668	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	61,677	17-Jun-98
	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	37,170	17-Jun-98
	GB_HTG1:HS24H01	46989	AL121632	Homo sapiens chromosome 21 clone LLNLc116H0124 map 21q21, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	19,820	29-Sep-99
rxa02596 1326	GB_BA1:MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome; segment 157/162.	Mycobacterium tuberculosis	36,957	24-Jun-99
	GB_BA2:AF026540	1778	AF026540	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	Mycobacterium tuberculosis	67,627	30-OCT-1998
	GB_BA2:MTU96128	1200	U96128	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	Mycobacterium tuberculosis	70,417	25-MAR-1998
rxa02611 1775	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	38,532	17-Jun-98
	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	60,575	10-DEC-1996
	GB_BA1:U00014	36470	U00014	Mycobacterium leprae cosmid B1549.	Mycobacterium leprae	57,486	29-Sep-94
rxa02612 2316	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	38,018	17-Jun-98
	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	58,510	10-DEC-1996
	GB_BA1:STMGLGEN	2557	L11647	Streptomyces aureofaciens glycogen branching enzyme (glgB) gene, complete cds.	Streptomyces aureofaciens	57,193	25-MAY-1995
rxa02621 942	GB_BA1:CGL133719	1839	AJ133719	Corynebacterium glutamicum yjcc gene, amtR gene and citE gene, partial.	Corynebacterium glutamicum	36,858	12-Aug-99
	GB_IN1:CEM106	39973	Z46935	Caenorhabditis elegans cosmid M106, complete sequence.	Caenorhabditis elegans	37,608	2-Sep-99
	GB_EST29:AI547662	377	AI547662	UI-R-C3-sz-h-03-0-UI.s1 UI-R-C3 Rattus norvegicus cDNA clone UI-R-C3-sz-h-03-0-UI 3', mRNA sequence.	Rattus norvegicus	50,667	3-Jul-99
rxa02640 1650	GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	39,187	24-Jun-99
	GB_BA1:PAU49666	4495	U49666	Pseudomonas aeruginosa (orfX), glycerol dfiffusion facilitator (glpF), glycerol kinase (glpK), and Glp repressor (glpR) genes, complete cds, and (orfK) gene, partial cds.	Pseudomonas aeruginosa	59,273	18-MAY-1997
	GB_BA1:AB015974	1641	AB015974	Pseudomonas tolaasii glpK gene for glycerol kinase, complete cds.	Pseudomonas tolaasii	58,339	28-Aug-99
rxa02654 1008	GB_EST6:N65787	512	N65787	20827 Lambda-PRL2 Arabidopsis thaliana cDNA clone 232B7T7, mRNA sequence.	Arabidopsis thaliana	39,637	5-Jan-98
	GB_PL2:T17H3	65839	AC005916	Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, complete sequence.	Arabidopsis thaliana	33,735	5-Aug-99
	GB_RO:MMU58105	88871	U58105	Mus musculus Btk locus, alpha-D-galactosidase A (Ags), ribosomal protein (L44L), and Bruton's tyrosine kinase (Btk) genes, complete cds.	Mus musculus	35,431	13-Feb-97
rxa02666 891	GB_PR3:AC004643	43411	AC004643	Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.	Homo sapiens	38,851	01-MAY-1998

Table 4 (continued)

	GB_PR3:AC004643	43411	AC004643	Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.	Homo sapiens	41,599	01-MAY-1998
	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	40,413	1-Jul-98
rxa02675 1980	GB_BA1:PDENQOURF	10425	L02354	Paracoccus denitrificans NADH dehydrogenase (URF4), (NQO8), (NQO9), (URF5), (URF6), (NQO10), (NQO11), (NQO12), (NQO13), and (NQO14) genes, complete cds's; biotin [acetyl-CoA carboxyl] ligase (birA) gene, complete cds.	Paracoccus denitrificans	40,735	20-MAY-1993
	GB_BA1:MTCY339	42861	Z77163	Mycobacterium tuberculosis H37Rv complete genome; segment 101/162.	Mycobacterium tuberculosis	36,471	17-Jun-98
	GB_BA1:MXADEVRS	2452	L19029	Myxococcus xanthus devR and devS genes, complete cds's.	Myxococcus xanthus	38,477	27-Jan-94
rxa02694 1065	GB_BA1:BACLDH	1147	M19394	B.caldolyticus lactate dehydrogenase (LDH) gene, complete cds.	Bacillus caldolyticus	57,371	26-Apr-93
	GB_BA1:BACLDHL	1361	M14788	B.stearothermophilus lct gene encoding L-lactate dehydrogenase, complete cds.	Bacillus stearothermophilus	57,277	26-Apr-93
	GB_PAT:A06664	1350	A06664	B.stearothermophilus lct gene.	Bacillus stearothermophilus	57,277	29-Jul-93
rxa02729 844	GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ;, mRNA sequence.	Danio rerio	50,746	27-Jun-97
	GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ;, mRNA sequence.	Danio rerio	36,364	27-Jun-97
rxa02730 1161	GB_EST19:AA758660	233	AA758660	ah67d06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320683 3', mRNA sequence.	Homo sapiens	37,059	29-DEC-1998
	GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ;, mRNA sequence.	Danio rerio	42,149	27-Jun-97
	GB_PR4:AC006285	150172	AC006285	Homo sapiens, complete sequence.	Homo sapiens	37,655	15-Nov-99
rxa02737 1665	GB_PAT:E13655	2260	E13655	gDNA encoding glucose-6-phosphate dehydrogenase.	Corynebacterium glutamicum	99,580	24-Jun-98
	GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	38,363	19-Jun-98
	GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	39,444	27-Jul-98
rxa02738 1203	GB_PAT:E13655	2260	E13655	gDNA encoding glucose-6-phosphate dehydrogenase.	Corynebacterium glutamicum	98,226	24-Jun-98
	GB_BA1:SCC22	22115	AL096839	Streptomyces coelicolor cosmid C22.	Streptomyces coelicolor	60,399	12-Jul-99
	GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	36,426	27-Jul-98
rxa02739 2223	GB_BA1:AB023377	2572	AB023377	Corynebacterium glutamicum tkt gene for transketolase, complete cds.	Corynebacterium glutamicum	99,640	20-Feb-99

Table 4 (continued)

		GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	61,573	04-DEC-1998
		GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	61,573	01-MAR-1994
rxa02740	1053	GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48I10 (D505) RPCI-98 48.I.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Drosophila melanogaster	37,105	2-Aug-99
		GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48I10 (D505) RPCI-98 48.I.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Drosophila melanogaster	37,105	2-Aug-99
		GB_HTG3:AC007150	121474	AC007150	Drosophila melanogaster chromosome 2 clone BACR16P13 (D597) RPCI-98 16.P.13 map 49E-49F strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 87 unordered pieces.	Drosophila melanogaster	38,728	20-Sep-99
rxa02741	1089	GB_HTG2:AC004951	129429	AC004951	Homo sapiens clone DJ1022I14, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.	Homo sapiens	33,116	12-Jun-98
		GB_HTG2:AC004951	129429	AC004951	Homo sapiens clone DJ1022I14, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.	Homo sapiens	33,116	12-Jun-98
		GB_IN1:AB006546	931	AB006546	Ephydatia fluviatilis mRNA for G protein a subunit 4, partial cds.	Ephydatia fluviatilis	36,379	23-Jun-99
rxa02743	1161	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	48,401	04-DEC-1998
		GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	48,401	01-MAR-1994
		GB_HTG2:AC007401	83657	AC007401	Homo sapiens clone NH0501O07, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	37,128	26-Jun-99
rxa02797	1026	GB_BA1:CGBETPGEN	2339	X93514	C.glutamicum betP gene.	Corynebacterium glutamicum	38,889	8-Sep-97
		GB_GSS9:AQ148714	405	AQ148714	HS_3136_A1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=5 Row=A, genomic survey sequence.	Homo sapiens	34,321	08-OCT-1998
		GB_BA1:BFU64514	3837	U64514	Bacillus firmus dppABC operon, dipeptide transporter protein dppA gene, partial cds, and dipeptide transporter proteins dppB and dppC genes, complete cds.	Bacillus firmus	38,072	1-Feb-97
rxa02803	680	GB_BA1:U00020	36947	U00020	Mycobacterium leprae cosmid B229.	Mycobacterium leprae	34,462	01-MAR-1994
		GB_BA2:PSU85643	4032	U85643	Pseudomonas syringae pv. syringae putative dihydropteroate synthase gene, partial cds, regulatory protein MrsA (mrsA), triose phosphate isomerase (tpiA), transport protein SecG (secG), tRNA-Leu, tRNA-Met, and 15 kDa protein genes, complete cds.	Pseudomonas syringae pv. syringae	50,445	9-Apr-97
		GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	59,314	20-Aug-98
rxa02821	363	GB_HTG2:AC008105	91421	AC008105	Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.	Homo sapiens	37,607	22-Jul-99
		GB_HTG2:AC008105	91421	AC008105	Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.	Homo sapiens	37,607	22-Jul-99
		GB_EST33:AV117143	222	AV117143	AV117143 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone 2610200J17, mRNA sequence.	Mus musculus	40,157	30-Jun-99

Table 4 (continued)

rxa02829	373	GB_HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LL0XNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	41,595	23-Nov-99
		GB_HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LL0XNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	41,595	23-Nov-99
		GB_PR3:HSU85B5	39550	Z69724	Human DNA sequence from cosmid U85B5, between markers DXS366 and DXS87 on chromosome X.	Homo sapiens	41,595	23-Nov-99
rxc03216	1141	GB_HTG3:AC008184	151720	AC008184	Drosophila melanogaster chromosome 2 clone BACR04D05 (D540) RPCI-98 04.D.5 map 36E5-36F2 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Drosophila melanogaster	39,600	2-Aug-99
		GB_EST15:AA477537	411	AA477537	zu36g12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740134 5' similar to contains Alu repetitive element;contains element HGR repetitive element ;, mRNA sequence.	Homo sapiens	37,260	9-Nov-97
		GB_EST26:AI330662	412	AI330662	fa91d08.y1 zebrafish fin day1 regeneration Danio rerio cDNA 5', mRNA sequence.	Danio rerio	37,805	28-DEC-1998
rxs03215	1038	GB_BA1:SC3F9	19830	AL023862	Streptomyces coelicolor cosmid 3F9.	Streptomyces coelicolor A3(2)	48,657	10-Feb-99
		GB_BA1:SLLINC	36270	X79146	S.lincolnensis (78-11) Lincomycin production genes.	Streptomyces lincolnensis	39,430	15-MAY-1996
		GB_HTG5:AC009660	204320	AC009660	Homo sapiens chromosome 15 clone RP11-424J10 map 15, *** SEQUENCING IN PROGRESS ***, 41 unordered pieces.	Homo sapiens	35,151	04-DEC-1999
rxs03224	1288	GB_PR3:AC004076	41322	AC004076	Homo sapiens chromosome 19, cosmid R30217, complete sequence.	Homo sapiens	37,788	29-Jan-98
		GB_PL2:SPAC926	23193	AL110469	S.pombe chromosome I cosmid c926.	Schizosaccharomyces pombe	38,474	2-Sep-99
		GB_BA2:AE001081	11473	AE001081	Archaeoglobus fulgidus section 26 of 172 of the complete genome.	Archaeoglobus fulgidus	35,871	15-DEC-1997

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose, 2.46 g/l $MgSO_4 \times 7H_2O$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(NH_4)_2SO_4$, 1 g/l NaCl, 2 g/l $MgSO_4 \times 7H_2O$, 0.2 g/l $CaCl_2$, 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $FeSO_4 \times H_2O$, 10 mg/l $ZnSO_4 \times 7\ H_2O$, 3 mg/l $MnCl_2 \times 4\ H_2O$, 30 mg/l H_3BO_3 20 mg/l $CoCl_2 \times 6\ H_2O$, 1 mg/l $NiCl_2 \times 6\ H_2O$, 3 mg/l $Na_2MoO_4 \times 2\ H_2O$, 500 mg/l complexing agent (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.,* Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see *e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g. Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli and C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.*

(1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other Corynebacterium or Brevibacterium species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) From Genes to Clones – Introduction to Gene Technology. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.*

(1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for Corynebacteria are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Procaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be

advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(NH_4)_2SO_4$, NH_4OH, nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It

is also possible to maintain a constant culture pH through the addition of NaOH or NH_4OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD_{600} of O.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be

found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) The Enzymes, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) Enzymkinetik, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example,

Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. Biochemical Engineering Fundamentals, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley and Sons; Fallon, A. *et al.* (1987) Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci.* USA 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci.* USA

90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to SMP nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to SMP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at http://www.gcg.com), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. John Wiley and Sons: New York). The gene sequences of the invention

were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label

may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as

described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18:

1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S-methionine, ^{35}S-cysteine, ^{14}C-labelled amino acids, ^{15}N-amino acids, $^{15}NO_3$ or $^{15}NH_4^+$ or ^{13}C-labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an SMP protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes an SMP protein involved in the production of a fine chemical.

3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing,, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.

9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.

10. A vector comprising the nucleic acid molecule of any one of claims 1-9.

11. The vector of claim 10, which is an expression vector.

12. A host cell transfected with the expression vector of claim 11.

13. The host cell of claim 12, wherein said cell is a microorganism.

14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium.*

15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.

16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.

18. An isolated SMP polypeptide from *Corynebacterium glutamicum*, or a portion thereof.

19. The polypeptide of claim 18, wherein said polypeptide is involved in the production of a fine chemical.

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.

23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those

sequences as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.

26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.

27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.

28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium.*

29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum, Corynebacterium herculis, Corynebacterium, lilium, Corynebacterium acetoacidophilum, Corynebacterium acetoglutamicum, Corynebacterium acetophilum, Corynebacterium ammoniagenes, Corynebacterium fujiokense, Corynebacterium nitrilophilus, Brevibacterium ammoniagenes, Brevibacterium butanicum, Brevibacterium divaricatum, Brevibacterium flavum, Brevibacterium healii, Brevibacterium ketoglutamicum, Brevibacterium ketosoreductum, Brevibacterium lactofermentum, Brevibacterium linens, Brevibacterium paraffinolyticum,* and those strains set forth in Table 3.

30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.

31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine

and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

32. The method of claim 25, wherein said fine chemical is an amino acid.

33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.

34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.

35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of SEQ ID NOs 1 through 782 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the nucleic acid molecule is disrupted.

35. 37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs in the Sequence Listing, wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listing s.

38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

SEQUENCE LISTING

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Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn Gly Phe Asp Leu His
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Leu Glu Lys Leu Ser Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile
     50                  55                  60

His Val Phe Phe Gly Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu
 65                  70                  75                  80

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            25                  30                  35

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        40                  45                  50

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70                  75                  80                  85

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                90                  95                  100

ggc ctg tgg ctg gaa gcg gga gcg aag ttc cct ggg tta aat           445
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10 15 20

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     55                  60                  65

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 70                  75                  80                  85

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150                 155                 160                 165

gag cgc ggt ctg aac acc gtc atc gag atc gac ggc ggc att agc gcc   643
Glu Arg Gly Leu Asn Thr Val Ile Glu Ile Asp Gly Gly Ile Ser Ala
                170                 175                 180

aag acc atc aag cag gct gcc gac gct ggc gtg gat gcc ttc gtt gca   691
Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val Asp Ala Phe Val Ala
            185                 190                 195

ggt tcc gct gtg tac ggc gct gag gat ccc aac aag gcg atc cag gag   739
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      50                  55                  60

Asp Val His Leu Met Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr
 65                  70                  75                  80

Ile Asp Ala Gly Ala Asp Cys Ile Val Phe His Val Glu Ala Thr Glu
                 85                  90                  95

Gly His Val Glu Leu Ala Lys Tyr Ile Arg Ser Lys Gly Val Arg Ala
            100                 105                 110

Gly Phe Ser Leu Arg Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp
        115                 120                 125

Leu Glu His Phe Asp Glu Val Ile Val Met Ser Val Glu Pro Gly Phe
    130                 135                 140

Gly Gly Gln Ser Phe Met Pro Glu Gln Leu Glu Lys Val Arg Thr Leu
145                 150                 155                 160

Arg Lys Val Ile Asp Glu Arg Gly Leu Asn Thr Val Ile Glu Ile Asp
                165                 170                 175

Gly Gly Ile Ser Ala Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val
            180                 185                 190

Asp Ala Phe Val Ala Gly Ser Ala Val Tyr Gly Ala Glu Asp Pro Asn
        195                 200                 205

Lys Ala Ile Gln Glu Leu Arg Ala Leu Ala Gln
    210                 215
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<210> 7
<211> 442
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXA01015

<400> 7

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ccaagattga gtcgagctat tttgcgattt gtgaaccccc aaatagggga aaagtccggg 60

tatccgccgt tgtgaaaatg cctgcagtaa actgacttcc atg cgc gta tac ctt   115
                                          Met Arg Val Tyr Leu
                                            1               5

gga gca gac cac gct ggt ttc gaa act aaa aat gca atc gca gaa cac   163
Gly Ala Asp His Ala Gly Phe Glu Thr Lys Asn Ala Ile Ala Glu His
                10                  15                  20

ctt aag gcc cac ggc cac gaa gtg atc gac tgc gga gcc cac acc tat   211
Leu Lys Ala His Gly His Glu Val Ile Asp Cys Gly Ala His Thr Tyr
```

```
            25                  30                  35

gat gca gaa gat gac tac cca gcc ttc tgc atc gaa gca gct agc cgc   259
Asp Ala Glu Asp Asp Tyr Pro Ala Phe Cys Ile Glu Ala Ala Ser Arg
         40                  45                  50

aca gta aac gac cca ggc tca ctc ggc atc gtc ctg ggt gga tcc gga   307
Thr Val Asn Asp Pro Gly Ser Leu Gly Ile Val Leu Gly Gly Ser Gly
     55                  60                  65

aac ggc gag cag atc gcc gcc aac aag gtc aag ggt gca cgt tgt gca   355
Asn Gly Glu Gln Ile Ala Ala Asn Lys Val Lys Gly Ala Arg Cys Ala
 70                  75                  80                  85

ctt gct tgg tct gtt gaa act gca cgc ctc gcc cgc gag cac aac aat   403
Leu Ala Trp Ser Val Glu Thr Ala Arg Leu Ala Arg Glu His Asn Asn
                 90                  95                 100

gcg aac ctc atc ggc atc ggc ggc cgc atg cac tca gag               442
Ala Asn Leu Ile Gly Ile Gly Gly Arg Met His Ser Glu
            105                 110
```

<210> 8
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 8

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Met Arg Val Tyr Leu Gly Ala Asp His Ala Gly Phe Glu Thr Lys Asn
  1               5                  10                  15

Ala Ile Ala Glu His Leu Lys Ala His Gly His Glu Val Ile Asp Cys
             20                  25                  30

Gly Ala His Thr Tyr Asp Ala Glu Asp Asp Tyr Pro Ala Phe Cys Ile
         35                  40                  45

Glu Ala Ala Ser Arg Thr Val Asn Asp Pro Gly Ser Leu Gly Ile Val
     50                  55                  60

Leu Gly Gly Ser Gly Asn Gly Glu Gln Ile Ala Ala Asn Lys Val Lys
 65                  70                  75                  80

Gly Ala Arg Cys Ala Leu Ala Trp Ser Val Glu Thr Ala Arg Leu Ala
                 85                  90                  95

Arg Glu His Asn Asn Ala Asn Leu Ile Gly Ile Gly Gly Arg Met His
            100                 105                 110

Ser Glu
```

<210> 9
<211> 2142
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(2119)
<223> RXN01312

<400> 9
gcagttgcgt acatcgttcc tgcactggtc ctgatcggca acatcaccat tccgttcgcc 60

atcgctgttg gttggattgc gtaaaggtta ggaagaattt atg agc act cac tct 115
Met Ser Thr His Ser
1 5

gaa acc acc cgc cca gag ttc atc cac cca gtc tca gtc ctc cca gag 163
Glu Thr Thr Arg Pro Glu Phe Ile His Pro Val Ser Val Leu Pro Glu
10 15 20

gtc tca gct ggt acg gtc ctt gac gct gca gag cca gca ggc gtt ccc 211
Val Ser Ala Gly Thr Val Leu Asp Ala Ala Glu Pro Ala Gly Val Pro
25 30 35

acc aaa gat atg tgg gaa tac caa aaa gac cac atg aac ctg gtc tcc 259
Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His Met Asn Leu Val Ser
40 45 50

cca ctg aac cga cgc aag ttc cgt gtc ctc gtc gtt ggc acc ggc ctg 307
Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val Val Gly Thr Gly Leu
55 60 65

tcc ggt ggt gct gca gca gca gcc ctc ggc gaa ctc gga tac gac gtc 355
Ser Gly Gly Ala Ala Ala Ala Ala Leu Gly Glu Leu Gly Tyr Asp Val
70 75 80 85

aag gcg ttc acc tac cac gac gca cct cgc cgt gcg cac tcc att gct 403
Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg Ala His Ser Ile Ala
90 95 100

gca cag ggt ggc gtt aac tcc gcc cgc ggc aag aag gta gac aac gac 451
Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys Lys Val Asp Asn Asp
105 110 115

ggc gca tac cgc cac gtc aag gac acc gtc aag ggc ggc gac tac cgt 499
Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys Gly Gly Asp Tyr Arg
120 125 130

ggt cgc gag tcc gac tgc tgg cgt ctc gcc gtc gag tcc gtc cgc gtc 547
Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val Glu Ser Val Arg Val
135 140 145

atc gac cac atg aac gcc atc ggt gca cca ttc gcc cgc gaa tac ggt 595
Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe Ala Arg Glu Tyr Gly
150 155 160 165

ggc gcc ttg gca acc cgt tcc ttc ggt ggt gtg cag gtc tcc cgt acc 643
Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val Gln Val Ser Arg Thr
170 175 180

tac tac acc cgt gga caa acc gga cag cag ctg cag ttc tcc acc gca 691
Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu Gln Phe Ser Thr Ala
185 190 195

tcc gca cta cag cgc cag atc cac ctc ggc tcc gta gaa atc ttc acc 739
Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser Val Glu Ile Phe Thr
200 205 210

```
cat aac gaa atg gtt gac gtc att gtc acc gaa cgt aac ggt gaa aag   787
His Asn Glu Met Val Asp Val Ile Val Thr Glu Arg Asn Gly Glu Lys
    215                 220                 225

cgc tgc gaa ggc ctg atc atg cgc aac ctg atc acc ggc gag ctc acc   835
Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile Thr Gly Glu Leu Thr
230                 235                 240                 245

gca cac acc ggc cat gcc gtt atc ctg gca acc ggt ggc tac ggc aac   883
Ala His Thr Gly His Ala Val Ile Leu Ala Thr Gly Gly Tyr Gly Asn
                250                 255                 260

gtg tac cac atg tcc acc ctg gcc aag aac tcc aac gcc tcg gcc atc   931
Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser Asn Ala Ser Ala Ile
            265                 270                 275

atg cgt gca tac gaa gcc ggc gca tac ttc gcg tcc cca tcg ttc atc   979
Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala Ser Pro Ser Phe Ile
        280                 285                 290

cag ttc cac cca acc ggc ctg cct gtg aac tcc acc tgg cag tcc aag   1027
Gln Phe His Pro Thr Gly Leu Pro Val Asn Ser Thr Trp Gln Ser Lys
    295                 300                 305

acc att ctg atg tcc gag tcg ctg cgt aac gac ggc cgc atc tgg tcc   1075
Thr Ile Leu Met Ser Glu Ser Leu Arg Asn Asp Gly Arg Ile Trp Ser
310                 315                 320                 325

cct aag gaa ccg aac gat aac cgc gat cca aac acc atc cct gag gat   1123
Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp
                330                 335                 340

gag cgc gac tac ttc ctg gag cgc cgc tac cca gca ttc ggt aac ctc   1171
Glu Arg Asp Tyr Phe Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu
            345                 350                 355

gtc cca cgt gac gtt gct tcc cgt gcg atc tcc cag cag atc aat gct   1219
Val Pro Arg Asp Val Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala
        360                 365                 370

ggt ctc ggt gtt gga cct ctg aac aac gct gca tac ctg gac ttc cgc   1267
Gly Leu Gly Val Gly Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg
    375                 380                 385

gac gcc acc gag cgc ctc gga cag gac acc atc cgc gag cgt tac tcc   1315
Asp Ala Thr Glu Arg Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser
390                 395                 400                 405

aac ctc ttc acc atg tac gaa gag gca att ggc gag gac cca tac tcc   1363
Asn Leu Phe Thr Met Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser
                410                 415                 420

agc cca atg cgt att gca ccg acc tgc cac ttc acc atg ggt ggc ctc   1411
Ser Pro Met Arg Ile Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu
            425                 430                 435

tgg act gac ttc aac gaa atg acg tca ctc cca ggt ctg ttc tgc gca   1459
Trp Thr Asp Phe Asn Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala
        440                 445                 450
```

```
ggc gaa gca tcc tgg acc tac cac ggt gca aac cgt ctg ggc gca aac   1507
Gly Glu Ala Ser Trp Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn
    455                 460                 465

tcc ctg ctc tcc gct tcc gtc gat ggc tgg ttc acc ctg cca ttc acc   1555
Ser Leu Leu Ser Ala Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr
470                 475                 480                 485

atc cct aac tac ctc ggc cca ttg ctt ggc tcc gag cgt ctg tca gag   1603
Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu
                490                 495                 500

gat gca cca gaa gca cag gca gcg att gcg cgt gca cag gct cgc att   1651
Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile
            505                 510                 515

gac cgc ctc atg ggc aac cgc cca gag tgg gtc ggt gac aac gtt cac   1699
Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val Gly Asp Asn Val His
        520                 525                 530

gga cct gag tac tac cac cgc cag ctt ggc gat atc ctg tac ttc tcc   1747
Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser
    535                 540                 545

tgt ggc gtt tcc cga aac gta gaa gac ctc cag gat ggc atc aac aag   1795
Cys Gly Val Ser Arg Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys
550                 555                 560                 565

atc cgt gcc ctc cgc gat gac ttc tgg aag aac atg cgc atc acc ggc   1843
Ile Arg Ala Leu Arg Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly
                570                 575                 580

agc acc gat gag atg aac cag gtt ctc gaa tac gca gca cgc gta gcc   1891
Ser Thr Asp Glu Met Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala
            585                 590                 595

gac tac atc gac ctc ggc gaa ctc atg tgt gtc gac gcc ctc gac cgc   1939
Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg
        600                 605                 610

gac gag tcc tgt ggc gct cac ttc cgc gac gac cac ctc tcc gaa gat   1987
Asp Glu Ser Cys Gly Ala His Phe Arg Asp Asp His Leu Ser Glu Asp
    615                 620                 625

ggc gaa gca caa cgt gac gac caa aac tgg tgc ttc gtc tcc gca tgg   2035
Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp
630                 635                 640                 645

gaa cca ggc gag aat gga acc ttc gtc tgc cac gca gaa cca ctg ttc   2083
Glu Pro Gly Glu Asn Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe
                650                 655                 660

ttc gaa tct gtc cca ctg cag aca agg aac tac aag taatgaaact        2129
Phe Glu Ser Val Pro Leu Gln Thr Arg Asn Tyr Lys
            665                 670

tacacttgag atc                                                   2142
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<210> 10
<211> 673

<212> PRT
<213> Corynebacterium glutamicum

<400> 10

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Met Ser Thr His Ser Glu Thr Thr Arg Pro Glu Phe Ile His Pro Val
  1               5                  10                  15

Ser Val Leu Pro Glu Val Ser Ala Gly Thr Val Leu Asp Ala Ala Glu
             20                  25                  30

Pro Ala Gly Val Pro Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His
         35                  40                  45

Met Asn Leu Val Ser Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val
     50                  55                  60

Val Gly Thr Gly Leu Ser Gly Gly Ala Ala Ala Ala Ala Leu Gly Glu
 65                  70                  75                  80

Leu Gly Tyr Asp Val Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg
                 85                  90                  95

Ala His Ser Ile Ala Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys
            100                 105                 110

Lys Val Asp Asn Asp Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys
        115                 120                 125

Gly Gly Asp Tyr Arg Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val
    130                 135                 140

Glu Ser Val Arg Val Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe
145                 150                 155                 160

Ala Arg Glu Tyr Gly Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val
                165                 170                 175

Gln Val Ser Arg Thr Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu
            180                 185                 190

Gln Phe Ser Thr Ala Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser
        195                 200                 205

Val Glu Ile Phe Thr His Asn Glu Met Val Asp Val Ile Val Thr Glu
    210                 215                 220

Arg Asn Gly Glu Lys Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile
225                 230                 235                 240

Thr Gly Glu Leu Thr Ala His Thr Gly His Ala Val Ile Leu Ala Thr
                245                 250                 255

Gly Gly Tyr Gly Asn Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser
            260                 265                 270

Asn Ala Ser Ala Ile Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala
        275                 280                 285

Ser Pro Ser Phe Ile Gln Phe His Pro Thr Gly Leu Pro Val Asn Ser
    290                 295                 300
```

```
Thr Trp Gln Ser Lys Thr Ile Leu Met Ser Glu Ser Leu Arg Asn Asp
305                 310                 315                 320

Gly Arg Ile Trp Ser Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn
                325                 330                 335

Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe Leu Glu Arg Arg Tyr Pro
            340                 345                 350

Ala Phe Gly Asn Leu Val Pro Arg Asp Val Ala Ser Arg Ala Ile Ser
        355                 360                 365

Gln Gln Ile Asn Ala Gly Leu Gly Val Gly Pro Leu Asn Asn Ala Ala
    370                 375                 380

Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg Leu Gly Gln Asp Thr Ile
385                 390                 395                 400

Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met Tyr Glu Glu Ala Ile Gly
                405                 410                 415

Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile Ala Pro Thr Cys His Phe
            420                 425                 430

Thr Met Gly Gly Leu Trp Thr Asp Phe Asn Glu Met Thr Ser Leu Pro
        435                 440                 445

Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp Thr Tyr His Gly Ala Asn
    450                 455                 460

Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala Ser Val Asp Gly Trp Phe
465                 470                 475                 480

Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser
                485                 490                 495

Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg
            500                 505                 510

Ala Gln Ala Arg Ile Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val
        515                 520                 525

Gly Asp Asn Val His Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp
    530                 535                 540

Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg Asn Val Glu Asp Leu Gln
545                 550                 555                 560

Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg Asp Asp Phe Trp Lys Asn
                565                 570                 575

Met Arg Ile Thr Gly Ser Thr Asp Glu Met Asn Gln Val Leu Glu Tyr
            580                 585                 590

Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val
        595                 600                 605

Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly Ala His Phe Arg Asp Asp
    610                 615                 620

His Leu Ser Glu Asp Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys
```

625 630 635 640

Phe Val Ser Ala Trp Glu Pro Gly Glu Asn Gly Thr Phe Val Cys His
645 650 655

Ala Glu Pro Leu Phe Phe Glu Ser Val Pro Leu Gln Thr Arg Asn Tyr
660 665 670

Lys

<210> 11
<211> 1100
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1077)
<223> FRXA01312

<400> 11
gag tcg ctg cgt aac gac ggc cgc atc tgg tcc cct aag gaa ccg aac 48
Glu Ser Leu Arg Asn Asp Gly Arg Ile Trp Ser Pro Lys Glu Pro Asn
1 5 10 15

gat aac cgc gat cca aac acc atc cct gag gat gag cgc gac tac ttc 96
Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe
20 25 30

ctg gag cgc cgc tac cca gca ttc ggt aac ctc gtc cca cgt gac gtt 144
Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu Val Pro Arg Asp Val
35 40 45

gct tcc cgt gcg atc tcc cag cag atc aat gct ggt ctc ggt gtt gga 192
Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala Gly Leu Gly Val Gly
50 55 60

cct ctg aac aac gct gca tac ctg gac ttc cgc gac gcc acc gag cgc 240
Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg
65 70 75 80

ctc gga cag gac acc atc cgc gag cgt tac tcc aac ctc ttc acc atg 288
Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met
85 90 95

tac gaa gag gca att ggc gag gac cca tac tcc agc cca atg cgt att 336
Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile
100 105 110

gca ccg acc tgc cac ttc acc atg ggt ggc ctc tgg act gac ttc aac 384
Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu Trp Thr Asp Phe Asn
115 120 125

gaa atg acg tca ctc cca ggt ctg ttc tgc gca ggc gaa gca tcc tgg 432
Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp
130 135 140

acc tac cac ggt gca aac cgt ctg ggc gca aac tcc ctg ctc tcc gct 480
Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala

```
145                 150                 155                 160

tcc gtc gat ggc tgg ttc acc ctg cca ttc acc atc cct aac tac ctc   528
Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu
                165                 170                 175

ggc cca ttg ctt ggc tcc gag cgt ctg tca gag gat gca cca gaa gca   576
Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala
            180                 185                 190

cag gca gcg att gcg cgt gca cag gct cgc att gac cgc ctc atg ggc   624
Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile Asp Arg Leu Met Gly
        195                 200                 205

aac cgc cca gag tgg gtc ggt gac aac gtt cac gga cct gag tac tac   672
Asn Arg Pro Glu Trp Val Gly Asp Asn Val His Gly Pro Glu Tyr Tyr
    210                 215                 220

cac cgc cag ctt ggc gat atc ctg tac ttc tcc tgt ggc gtt tcc cga   720
His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg
225                 230                 235                 240

aac gta gaa gac ctc cag gat ggc atc aac aag atc cgt gcc ctc cgc   768
Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg
                245                 250                 255

gat gac ttc tgg aag aac atg cgc atc acc ggc agc acc gat gag atg   816
Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met
            260                 265                 270

aac cag gtt ctc gaa tac gca gca cgc gta gcc gac tac atc gac ctc   864
Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu
        275                 280                 285

ggc gaa ctc atg tgt gtc gac gcc ctc gac cgc gac gag tcc tgt ggc   912
Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly
    290                 295                 300

gct cac ttc cgc gac gac cac ctc tcc gaa gat ggc gaa gca caa cgt   960
Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg
305                 310                 315                 320

gac gac caa aac tgg tgc ttc gtc tcc gca tgg gaa cca ggc gag aat  1008
Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn
                325                 330                 335

gga acc ttc gtc tgc cac gca gaa cca ctg ttc ttc gaa tct gtc cca  1056
Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe Phe Glu Ser Val Pro
            340                 345                 350

ctg cag aca agg aac tac aag taatgaaact tacacttgag atc           1100
Leu Gln Thr Arg Asn Tyr Lys
        355
```

<210> 12
<211> 359
<212> PRT
<213> Corynebacterium glutamicum

<400> 12

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Glu Ser Leu Arg Asn Asp Gly Arg Ile Trp Ser Pro Lys Glu Pro Asn
 1               5                  10                  15

Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe
            20                  25                  30

Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu Val Pro Arg Asp Val
        35                  40                  45

Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala Gly Leu Gly Val Gly
    50                  55                  60

Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg
65                  70                  75                  80

Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met
                85                  90                  95

Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile
            100                 105                 110

Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu Trp Thr Asp Phe Asn
        115                 120                 125

Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp
    130                 135                 140

Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala
145                 150                 155                 160

Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu
                165                 170                 175

Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala
            180                 185                 190

Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile Asp Arg Leu Met Gly
        195                 200                 205

Asn Arg Pro Glu Trp Val Gly Asp Asn Val His Gly Pro Glu Tyr Tyr
    210                 215                 220

His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg
225                 230                 235                 240

Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg
                245                 250                 255

Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met
            260                 265                 270

Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu
        275                 280                 285

Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly
    290                 295                 300

Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg
305                 310                 315                 320

Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn
```

```
                325                 330                 335

Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe Phe Glu Ser Val Pro
            340                 345                 350

Leu Gln Thr Arg Asn Tyr Lys
        355
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<210> 13
<211> 1593
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1570)
<223> RXN00231

<400> 13

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caggactacc tcgacgccgg cgccaacttt gtccgagtcg gtgccgatgt ccagcaactc 60

aacgctgctg gatacgaaaa gtgaaggaaa ataacgcatc atg act att aat gtt   115
                                            Met Thr Ile Asn Val
                                              1               5

ttc gaa cta ctt gtc aaa agt ccc acg ggt cta ctg att ggt gat tcc   163
Phe Glu Leu Leu Val Lys Ser Pro Thr Gly Leu Leu Ile Gly Asp Ser
                 10                  15                  20

tgg gtg gaa gca tcc gac ggc ggt act ttc gat gtg gaa aac cca gcg   211
Trp Val Glu Ala Ser Asp Gly Gly Thr Phe Asp Val Glu Asn Pro Ala
             25                  30                  35

acg ggt gaa aca atc gca acg ctc gcg tct gct act tcc gag gat gca   259
Thr Gly Glu Thr Ile Ala Thr Leu Ala Ser Ala Thr Ser Glu Asp Ala
         40                  45                  50

ctg gct gct ctt gat gct gca tgc gct gtt cag gcc gag tgg gct agg   307
Leu Ala Ala Leu Asp Ala Ala Cys Ala Val Gln Ala Glu Trp Ala Arg
     55                  60                  65

atg cca gcg cgc gag cgt tct aat att tta cgc cgc ggt ttt gag ctc   355
Met Pro Ala Arg Glu Arg Ser Asn Ile Leu Arg Arg Gly Phe Glu Leu
 70                  75                  80                  85

gta gca gaa cgt gca gaa gag ttc gcc acc ctc atg acc ttg gaa atg   403
Val Ala Glu Arg Ala Glu Glu Phe Ala Thr Leu Met Thr Leu Glu Met
                 90                  95                 100

ggc aag cct ttg gct gaa gct cgc ggc gaa gtc acc tac ggc aac gaa   451
Gly Lys Pro Leu Ala Glu Ala Arg Gly Glu Val Thr Tyr Gly Asn Glu
            105                 110                 115

ttc ctg cgc tgg ttc tct gag gaa gca gtt cgt ctg tat ggc cgt tac   499
Phe Leu Arg Trp Phe Ser Glu Glu Ala Val Arg Leu Tyr Gly Arg Tyr
        120                 125                 130

gga acc aca cca gaa ggc aac ttg cgg atg ctg acc gcc ctc aag cca   547
Gly Thr Thr Pro Glu Gly Asn Leu Arg Met Leu Thr Ala Leu Lys Pro
    135                 140                 145
```

```
gtt ggc ccg tgc ctc ctg atc acc cca tgg aac ttc cca cta gca atg   595
Val Gly Pro Cys Leu Leu Ile Thr Pro Trp Asn Phe Pro Leu Ala Met
150                 155                 160                 165

gct acc cgc aag gtc gca cct gcg atc gct gca ggt tgt gtc atg gtg   643
Ala Thr Arg Lys Val Ala Pro Ala Ile Ala Ala Gly Cys Val Met Val
                170                 175                 180

ctc aag cca gct cga ctt acc ccg ctg acc tcc cag tat ttt gct cag   691
Leu Lys Pro Ala Arg Leu Thr Pro Leu Thr Ser Gln Tyr Phe Ala Gln
            185                 190                 195

acc atg ctt gat gcc ggt ctt cca gca ggt gtc ctc aat gtg gtc tcc   739
Thr Met Leu Asp Ala Gly Leu Pro Ala Gly Val Leu Asn Val Val Ser
        200                 205                 210

ggt gct tcc gcc tct gcg att tcc aac ccg att atg gaa gac gat cgc   787
Gly Ala Ser Ala Ser Ala Ile Ser Asn Pro Ile Met Glu Asp Asp Arg
    215                 220                 225

ctt cgt aaa gtc tcc ttc acc ggc tcc acc cca gtt ggc cag cag ctg   835
Leu Arg Lys Val Ser Phe Thr Gly Ser Thr Pro Val Gly Gln Gln Leu
230                 235                 240                 245

ctc aaa aag gct gcc gat aaa gtt ctg cgc acc tcc atg gaa ctt ggt   883
Leu Lys Lys Ala Ala Asp Lys Val Leu Arg Thr Ser Met Glu Leu Gly
                250                 255                 260

ggc aac gca cct ttc att gtc ttc gag gac gcc gac cta gat ctc gcg   931
Gly Asn Ala Pro Phe Ile Val Phe Glu Asp Ala Asp Leu Asp Leu Ala
            265                 270                 275

atc gaa ggt gcc atg ggt gcc aaa atg cgc aac atc ggc gaa gct tgc   979
Ile Glu Gly Ala Met Gly Ala Lys Met Arg Asn Ile Gly Glu Ala Cys
        280                 285                 290

acc gca gcc aac cgt ttc tta gtc cac gaa tcc gtc gcc gat gaa ttc   1027
Thr Ala Ala Asn Arg Phe Leu Val His Glu Ser Val Ala Asp Glu Phe
    295                 300                 305

ggc cgt cgc ttc gct gcc cgc ctt gaa gag caa gtc cta ggc aac ggc   1075
Gly Arg Arg Phe Ala Ala Arg Leu Glu Glu Gln Val Leu Gly Asn Gly
310                 315                 320                 325

ctc gac gaa ggc gtc acc gtg ggc ccc ctg gtt gag gaa aaa gca cga   1123
Leu Asp Glu Gly Val Thr Val Gly Pro Leu Val Glu Glu Lys Ala Arg
                330                 335                 340

gac agc gtt gca tcg ctt gtc gac gcc gcc gtc gcc gaa ggt gcc acc   1171
Asp Ser Val Ala Ser Leu Val Asp Ala Ala Val Ala Glu Gly Ala Thr
            345                 350                 355

gtc ctc acc ggc ggc aag gcc ggc aca ggt gca ggc tac ttc tac gaa   1219
Val Leu Thr Gly Gly Lys Ala Gly Thr Gly Ala Gly Tyr Phe Tyr Glu
        360                 365                 370

cca acg gtg ctc acg gga gtt tca aca gat gcg gct atc ctg aac gaa   1267
Pro Thr Val Leu Thr Gly Val Ser Thr Asp Ala Ala Ile Leu Asn Glu
    375                 380                 385
```

```
gag atc ttc ggt ccc gtc gca ccg atc gtc acc ttc caa acc gag gaa   1315
Glu Ile Phe Gly Pro Val Ala Pro Ile Val Thr Phe Gln Thr Glu Glu
390                 395                 400                 405

gaa gcc ctg cgt cta gcc aac tcc acc gaa tac gga ctg gcc tcc tat   1363
Glu Ala Leu Arg Leu Ala Asn Ser Thr Glu Tyr Gly Leu Ala Ser Tyr
                410                 415                 420

gtg ttc acc cag gac acc tca cgt att ttc cgc gtc tcc gat ggt ctc   1411
Val Phe Thr Gln Asp Thr Ser Arg Ile Phe Arg Val Ser Asp Gly Leu
            425                 430                 435

gag ttc ggc cta gtg ggc gtc aat tcc ggt gtc atc tct aac gct gct   1459
Glu Phe Gly Leu Val Gly Val Asn Ser Gly Val Ile Ser Asn Ala Ala
        440                 445                 450

gca cct ttt ggt ggc gta aaa caa tcc gga atg ggc cgc gaa ggt ggt   1507
Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Met Gly Arg Glu Gly Gly
    455                 460                 465

ctc gaa gga atc gag gag tac acc tcc gtg cag tac atc ggt atc cgg   1555
Leu Glu Gly Ile Glu Glu Tyr Thr Ser Val Gln Tyr Ile Gly Ile Arg
470                 475                 480                 485

gat cct tac gcc ggc tagcatctgc ccctttacaa atc                    1593
Asp Pro Tyr Ala Gly
                490
```

<210> 14
<211> 490
<212> PRT
<213> Corynebacterium glutamicum

<400> 14

```
Met Thr Ile Asn Val Phe Glu Leu Leu Val Lys Ser Pro Thr Gly Leu
  1               5                  10                  15

Leu Ile Gly Asp Ser Trp Val Glu Ala Ser Asp Gly Gly Thr Phe Asp
             20                  25                  30

Val Glu Asn Pro Ala Thr Gly Glu Thr Ile Ala Thr Leu Ala Ser Ala
         35                  40                  45

Thr Ser Glu Asp Ala Leu Ala Ala Leu Asp Ala Ala Cys Ala Val Gln
     50                  55                  60

Ala Glu Trp Ala Arg Met Pro Ala Arg Glu Arg Ser Asn Ile Leu Arg
 65                  70                  75                  80

Arg Gly Phe Glu Leu Val Ala Glu Arg Ala Glu Glu Phe Ala Thr Leu
                 85                  90                  95

Met Thr Leu Glu Met Gly Lys Pro Leu Ala Glu Ala Arg Gly Glu Val
            100                 105                 110

Thr Tyr Gly Asn Glu Phe Leu Arg Trp Phe Ser Glu Glu Ala Val Arg
        115                 120                 125

Leu Tyr Gly Arg Tyr Gly Thr Thr Pro Glu Gly Asn Leu Arg Met Leu
    130                 135                 140
```

```
Thr Ala Leu Lys Pro Val Gly Pro Cys Leu Leu Ile Thr Pro Trp Asn
145                 150                 155                 160

Phe Pro Leu Ala Met Ala Thr Arg Lys Val Ala Pro Ala Ile Ala Ala
                165                 170                 175

Gly Cys Val Met Val Leu Lys Pro Ala Arg Leu Thr Pro Leu Thr Ser
            180                 185                 190

Gln Tyr Phe Ala Gln Thr Met Leu Asp Ala Gly Leu Pro Ala Gly Val
        195                 200                 205

Leu Asn Val Val Ser Gly Ala Ser Ala Ser Ala Ile Ser Asn Pro Ile
    210                 215                 220

Met Glu Asp Asp Arg Leu Arg Lys Val Ser Phe Thr Gly Ser Thr Pro
225                 230                 235                 240

Val Gly Gln Gln Leu Leu Lys Lys Ala Ala Asp Lys Val Leu Arg Thr
                245                 250                 255

Ser Met Glu Leu Gly Gly Asn Ala Pro Phe Ile Val Phe Glu Asp Ala
            260                 265                 270

Asp Leu Asp Leu Ala Ile Glu Gly Ala Met Gly Ala Lys Met Arg Asn
        275                 280                 285

Ile Gly Glu Ala Cys Thr Ala Ala Asn Arg Phe Leu Val His Glu Ser
    290                 295                 300

Val Ala Asp Glu Phe Gly Arg Arg Phe Ala Ala Arg Leu Glu Glu Gln
305                 310                 315                 320

Val Leu Gly Asn Gly Leu Asp Glu Gly Val Thr Val Gly Pro Leu Val
                325                 330                 335

Glu Glu Lys Ala Arg Asp Ser Val Ala Ser Leu Val Asp Ala Ala Val
            340                 345                 350

Ala Glu Gly Ala Thr Val Leu Thr Gly Gly Lys Ala Gly Thr Gly Ala
        355                 360                 365

Gly Tyr Phe Tyr Glu Pro Thr Val Leu Thr Gly Val Ser Thr Asp Ala
    370                 375                 380

Ala Ile Leu Asn Glu Glu Ile Phe Gly Pro Val Ala Pro Ile Val Thr
385                 390                 395                 400

Phe Gln Thr Glu Glu Glu Ala Leu Arg Leu Ala Asn Ser Thr Glu Tyr
                405                 410                 415

Gly Leu Ala Ser Tyr Val Phe Thr Gln Asp Thr Ser Arg Ile Phe Arg
            420                 425                 430

Val Ser Asp Gly Leu Glu Phe Gly Leu Val Gly Val Asn Ser Gly Val
        435                 440                 445

Ile Ser Asn Ala Ala Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Met
    450                 455                 460
```

```
Gly Arg Glu Gly Gly Leu Glu Gly Ile Glu Glu Tyr Thr Ser Val Gln
465                 470                 475                 480

Tyr Ile Gly Ile Arg Asp Pro Tyr Ala Gly
                485                 490


<210> 15
<211> 870
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(847)
<223> RXA01311

<400> 15
tcgtctccgc atgggaacca ggcgagaatg gaaccttcgt ctgccacgca gaaccactgt 60

tcttcgaatc tgtcccactg cagacaagga actacaagta atg aaa ctt aca ctt   115
                                              Met Lys Leu Thr Leu
                                                1               5

gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc   163
Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr
                10                  15                  20

gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt   211
Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu
            25                  30                  35

gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg   259
Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala
        40                  45                  50

ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc   307
Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu
    55                  60                  65

gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg   355
Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala
70                  75                  80                  85

cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca   403
Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro
                90                  95                  100

ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc   451
Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg
            105                 110                 115

tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac   499
Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn
        120                 125                 130

gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc   547
Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr
    135                 140                 145

gca gaa ctc gca ctt gac cac gca gcc tgc atc ggc tgt ggc gca tgt   595
```

```
Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys
150                 155                 160                 165

gtt gct gcc tgc cct aac ggc gca gca cac ctg ttc acc ggc gca aag   643
Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys
                170                 175                 180

ctt gtt cac ctc tcc ctc ctc cca ctg ggt aag gaa gag cgc gga ctg   691
Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu
            185                 190                 195

cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc   739
Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys
        200                 205                 210

tcc ctc tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg   787
Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu
    215                 220                 225

acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga   835
Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg
230                 235                 240                 245

ggc aaa gac gac tagtctttaa tccaagtaag tac                        870
Gly Lys Asp Asp
```

<210> 16
<211> 249
<212> PRT
<213> Corynebacterium glutamicum

<400> 16

```
Met Lys Leu Thr Leu Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu
  1               5                  10                  15

Gly Lys Phe Glu Thr Val Gln Val Asp Asp Ala Val Ala Gln Met Ser
             20                  25                  30

Ile Leu Glu Leu Leu Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly
         35                  40                  45

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly
     50                  55                  60

Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn
 65                  70                  75                  80

Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr
                 85                  90                  95

Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp
            100                 105                 110

Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly
        115                 120                 125

Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His
    130                 135                 140
```

```
Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile
145                 150                 155                 160

Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu
                165                 170                 175

Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys
            180                 185                 190

Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr
        195                 200                 205

Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro
    210                 215                 220

Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala
225                 230                 235                 240

Arg Ala Ala Phe Arg Gly Lys Asp Asp
                245
```

<210> 17
<211> 1530
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1507)
<223> RXA01535

<400> 17

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acccacctca ctctaggggt ggactccagt gtttcgcgac aacacaatga gtaagcttgt 60

gacagccgta tttaattctc agtaagaaat gagtgatttc atg acc gag cag gaa   115
                                            Met Thr Glu Gln Glu
                                              1               5

ttc cgt att gag cac gac acc atg ggt gaa gtg aag gtt cca gca aag   163
Phe Arg Ile Glu His Asp Thr Met Gly Glu Val Lys Val Pro Ala Lys
                10                  15                  20

gct ctg tgg cag gca cag acc cag cgc gct gtt gag aac ttc cct atc   211
Ala Leu Trp Gln Ala Gln Thr Gln Arg Ala Val Glu Asn Phe Pro Ile
            25                  30                  35

tct ggt cgt ggt ctg gaa tcc gca cag atc cgc gca atg ggt ctg ctg   259
Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg Ala Met Gly Leu Leu
        40                  45                  50

aag gca gct tgt gcg cag gta aac aag gac tcc ggt gcg ctg gat gca   307
Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser Gly Ala Leu Asp Ala
    55                  60                  65

gag aag gca gat gcc atc att gca gct ggt aag gag atc gcg tcc ggt   355
Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys Glu Ile Ala Ser Gly
70                  75                  80                  85

aag cat gac gct gag ttc cca att gat gtg ttc cag act ggt tcc ggt   403
Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe Gln Thr Gly Ser Gly
```

```
                90                  95                 100

act tcc tcc aac atg aac acc aat gag gtt atc gct tcc atc gcg aag   451
Thr Ser Ser Asn Met Asn Thr Asn Glu Val Ile Ala Ser Ile Ala Lys
            105                 110                 115

gct aac ggc gtt gag gtt cac cca aat gac cac gtc aac atg ggt cag   499
Ala Asn Gly Val Glu Val His Pro Asn Asp His Val Asn Met Gly Gln
        120                 125                 130

tcc tcc aat gac acc ttc cct act gca act cac gtt gct gca acc gaa   547
Ser Ser Asn Asp Thr Phe Pro Thr Ala Thr His Val Ala Ala Thr Glu
    135                 140                 145

gct gct gtc aat gac ctc atc cca ggc ctg aag gtt ctg cac gag tct   595
Ala Ala Val Asn Asp Leu Ile Pro Gly Leu Lys Val Leu His Glu Ser
150                 155                 160                 165

ttg gcg aag aag gct aac gag tgg tct gag gtt gtt aag tcc ggc cgc   643
Leu Ala Lys Lys Ala Asn Glu Trp Ser Glu Val Val Lys Ser Gly Arg
                170                 175                 180

acc cac ctg atg gac gct gtt cca gta acc ctg ggc cag gag ttc ggt   691
Thr His Leu Met Asp Ala Val Pro Val Thr Leu Gly Gln Glu Phe Gly
            185                 190                 195

ggc tac gct cgc cag atc cag ctc ggc atc gag cgc gtt gag gct act   739
Gly Tyr Ala Arg Gln Ile Gln Leu Gly Ile Glu Arg Val Glu Ala Thr
        200                 205                 210

ctt cct cgc ctt ggt gag ctg gct att ggt ggc acc gct gct ggt acc   787
Leu Pro Arg Leu Gly Glu Leu Ala Ile Gly Gly Thr Ala Ala Gly Thr
    215                 220                 225

ggt atc aac acc tcc gct gat ttc ggc ggc aag gtt gtt gct gaa ctg   835
Gly Ile Asn Thr Ser Ala Asp Phe Gly Gly Lys Val Val Ala Glu Leu
230                 235                 240                 245

atc aac ttg acc gac gtc aag gag ctc aag gaa gct gag aac cac ttc   883
Ile Asn Leu Thr Asp Val Lys Glu Leu Lys Glu Ala Glu Asn His Phe
                250                 255                 260

gag gct cag gct gca cgc gac gct ctt gtt gag ttc tcc ggc gca atg   931
Glu Ala Gln Ala Ala Arg Asp Ala Leu Val Glu Phe Ser Gly Ala Met
            265                 270                 275

cgc gtt atc gct gtc tcc ttg tac aag atc gct aac gat atc cgc ctc   979
Arg Val Ile Ala Val Ser Leu Tyr Lys Ile Ala Asn Asp Ile Arg Leu
        280                 285                 290

atg ggc tcc ggc cca ctg acc ggt ctt ggc gag atc cgt ctc cca gac   1027
Met Gly Ser Gly Pro Leu Thr Gly Leu Gly Glu Ile Arg Leu Pro Asp
    295                 300                 305

ctg cag cca ggt tcc tcc atc atg cca ggc aag gtc aac cca gtt ctc   1075
Leu Gln Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Leu
310                 315                 320                 325

tgt gag acc gct acc cag gtt tcc gct cag gtt atc ggc aat gac gca   1123
Cys Glu Thr Ala Thr Gln Val Ser Ala Gln Val Ile Gly Asn Asp Ala
                330                 335                 340
```

```
gct gtt gcg ttc tcc ggc acc cag ggc cag ttc gag ctc aac gtg ttc   1171
Ala Val Ala Phe Ser Gly Thr Gln Gly Gln Phe Glu Leu Asn Val Phe
            345                 350                 355

atc cca gtg atg gct cgc aac gtg ctt gag tcc gct cgc ctg ctg gct   1219
Ile Pro Val Met Ala Arg Asn Val Leu Glu Ser Ala Arg Leu Leu Ala
        360                 365                 370

aac act tcc cgc gtg ttc gca acc cgt ctc gtt gat ggc att gag cca   1267
Asn Thr Ser Arg Val Phe Ala Thr Arg Leu Val Asp Gly Ile Glu Pro
    375                 380                 385

aac gag gca cac atg aag gag ctc gct gag tct tca cct tcc atc gtt   1315
Asn Glu Ala His Met Lys Glu Leu Ala Glu Ser Ser Pro Ser Ile Val
390                 395                 400                 405

acc cca ctg aac tct gca atc ggc tac gaa gct gct gca aag gtg gct   1363
Thr Pro Leu Asn Ser Ala Ile Gly Tyr Glu Ala Ala Ala Lys Val Ala
                410                 415                 420

aag act gct ttg gct gag ggc aag acc atc cgc cag act gtc atc gat   1411
Lys Thr Ala Leu Ala Glu Gly Lys Thr Ile Arg Gln Thr Val Ile Asp
            425                 430                 435

ttg ggc ttg gtt gat ggc gag aag ctc acc gag gaa gag ctg gac aag   1459
Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu Glu Glu Leu Asp Lys
        440                 445                 450

cgc ctc gac gtt ctt gct atg gct cac acc gag cgc gag aac aag ttc   1507
Arg Leu Asp Val Leu Ala Met Ala His Thr Glu Arg Glu Asn Lys Phe
    455                 460                 465

taaaactaga acccgataaa taa                                        1530
```

<210> 18
<211> 469
<212> PRT
<213> Corynebacterium glutamicum

<400> 18

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Met Thr Glu Gln Glu Phe Arg Ile Glu His Asp Thr Met Gly Glu Val
  1               5                  10                  15

Lys Val Pro Ala Lys Ala Leu Trp Gln Ala Gln Thr Gln Arg Ala Val
             20                  25                  30

Glu Asn Phe Pro Ile Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg
         35                  40                  45

Ala Met Gly Leu Leu Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser
     50                  55                  60

Gly Ala Leu Asp Ala Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys
 65                  70                  75                  80

Glu Ile Ala Ser Gly Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe
                 85                  90                  95

Gln Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Thr Asn Glu Val Ile
```

```
            100                 105                 110

Ala Ser Ile Ala Lys Ala Asn Gly Val Glu Val His Pro Asn Asp His
        115                 120                 125

Val Asn Met Gly Gln Ser Ser Asn Asp Thr Phe Pro Thr Ala Thr His
    130                 135                 140

Val Ala Ala Thr Glu Ala Ala Val Asn Asp Leu Ile Pro Gly Leu Lys
145                 150                 155                 160

Val Leu His Glu Ser Leu Ala Lys Lys Ala Asn Glu Trp Ser Glu Val
                165                 170                 175

Val Lys Ser Gly Arg Thr His Leu Met Asp Ala Val Pro Val Thr Leu
            180                 185                 190

Gly Gln Glu Phe Gly Gly Tyr Ala Arg Gln Ile Gln Leu Gly Ile Glu
        195                 200                 205

Arg Val Glu Ala Thr Leu Pro Arg Leu Gly Glu Leu Ala Ile Gly Gly
    210                 215                 220

Thr Ala Ala Gly Thr Gly Ile Asn Thr Ser Ala Asp Phe Gly Gly Lys
225                 230                 235                 240

Val Val Ala Glu Leu Ile Asn Leu Thr Asp Val Lys Glu Leu Lys Glu
                245                 250                 255

Ala Glu Asn His Phe Glu Ala Gln Ala Ala Arg Asp Ala Leu Val Glu
            260                 265                 270

Phe Ser Gly Ala Met Arg Val Ile Ala Val Ser Leu Tyr Lys Ile Ala
        275                 280                 285

Asn Asp Ile Arg Leu Met Gly Ser Gly Pro Leu Thr Gly Leu Gly Glu
    290                 295                 300

Ile Arg Leu Pro Asp Leu Gln Pro Gly Ser Ser Ile Met Pro Gly Lys
305                 310                 315                 320

Val Asn Pro Val Leu Cys Glu Thr Ala Thr Gln Val Ser Ala Gln Val
                325                 330                 335

Ile Gly Asn Asp Ala Ala Val Ala Phe Ser Gly Thr Gln Gly Gln Phe
            340                 345                 350

Glu Leu Asn Val Phe Ile Pro Val Met Ala Arg Asn Val Leu Glu Ser
        355                 360                 365

Ala Arg Leu Leu Ala Asn Thr Ser Arg Val Phe Ala Thr Arg Leu Val
    370                 375                 380

Asp Gly Ile Glu Pro Asn Glu Ala His Met Lys Glu Leu Ala Glu Ser
385                 390                 395                 400

Ser Pro Ser Ile Val Thr Pro Leu Asn Ser Ala Ile Gly Tyr Glu Ala
                405                 410                 415

Ala Ala Lys Val Ala Lys Thr Ala Leu Ala Glu Gly Lys Thr Ile Arg
            420                 425                 430
```

```
Gln Thr Val Ile Asp Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu
        435                 440                 445

Glu Glu Leu Asp Lys Arg Leu Asp Val Leu Ala Met Ala His Thr Glu
    450                 455                 460

Arg Glu Asn Lys Phe
465
```

<210> 19
<211> 1164
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1141)
<223> RXA00517

<400> 19

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ggtcttagaa ccagcgtgca ctgatggcga ttaaaggggg ttgcgcctat acctattgct 60

ggtatacatt tcggtatacc taaaccgaat tgagggattc atg cca gaa gtc act   115
                                            Met Pro Glu Val Thr
                                              1               5

gtc aac gcc caa caa ctc act gtt ctc tgc aca gac atc ctc acc aaa   163
Val Asn Ala Gln Gln Leu Thr Val Leu Cys Thr Asp Ile Leu Thr Lys
                10                  15                  20

act gga gta cct gca gca gac gcc cat ctt gtc ggt gat agt ttg gtg   211
Thr Gly Val Pro Ala Ala Asp Ala His Leu Val Gly Asp Ser Leu Val
            25                  30                  35

cag gct gat ctt tgg ggt cac ccc tcc cac ggt gtg ctt cga ctg cct   259
Gln Ala Asp Leu Trp Gly His Pro Ser His Gly Val Leu Arg Leu Pro
        40                  45                  50

tgg tat gtg cgc aga ctc cac agt ggc gcg atg act aca cat gca cac   307
Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met Thr Thr His Ala His
    55                  60                  65

gtg gag gtt ctc aat gat ttg ggt gcc gtg ttg gcg ttg gat gga cac   355
Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu Ala Leu Asp Gly His
70                  75                  80                  85

aat gga atc ggc caa gtt tta gct gat cat gct cgt aaa gaa gca gtg   403
Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala Arg Lys Glu Ala Val
                90                  95                  100

act agg gca atg atg ttc ggc atc ggt gcg gtg tcg gtg cgc aac tcc   451
Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val Ser Val Arg Asn Ser
            105                 110                 115

aat cat ttt gga act gcc atg tac tac acc cgg aaa gcg gca gcg caa   499
Asn His Phe Gly Thr Ala Met Tyr Tyr Thr Arg Lys Ala Ala Ala Gln
        120                 125                 130

gga tgt gtt tcc att ctc acc acc aat gca tct ccg gcg atg gcg ccc   547
```

```
Gly Cys Val Ser Ile Leu Thr Thr Asn Ala Ser Pro Ala Met Ala Pro
    135                 140                 145

tgg ggt ggc aga gaa aaa cgg atc ggt acc aac cca tgg tct att gcg   595
Trp Gly Gly Arg Glu Lys Arg Ile Gly Thr Asn Pro Trp Ser Ile Ala
150                 155                 160                 165

gca cct ttt gga gaa acg gct acg gta gtc gat ata gcc aat act gcg   643
Ala Pro Phe Gly Glu Thr Ala Thr Val Val Asp Ile Ala Asn Thr Ala
                170                 175                 180

gtt gcg cgc gga aag atc tac cac gca cga cag aca aac atg ccc att   691
Val Ala Arg Gly Lys Ile Tyr His Ala Arg Gln Thr Asn Met Pro Ile
            185                 190                 195

cct gag act tgg gcg atc acg agt gag ggc gca ccc acc acg gat cct   739
Pro Glu Thr Trp Ala Ile Thr Ser Glu Gly Ala Pro Thr Thr Asp Pro
        200                 205                 210

gct gag gca atc aac ggt gtc gtc ctt ccc atg gct ggt cac aaa ggt   787
Ala Glu Ala Ile Asn Gly Val Val Leu Pro Met Ala Gly His Lys Gly
    215                 220                 225

tat gcg att agc ttc atg atg gat gtg ctt tct gga gtt ctc act ggt   835
Tyr Ala Ile Ser Phe Met Met Asp Val Leu Ser Gly Val Leu Thr Gly
230                 235                 240                 245

tcc cag cac agc acc aag gta cat ggt ccg tat gat ccc act ccc cca   883
Ser Gln His Ser Thr Lys Val His Gly Pro Tyr Asp Pro Thr Pro Pro
                250                 255                 260

ggt gga gct ggc cac ttg ttc atc gcg ttg gat gtt gca gcg ttt cgc   931
Gly Gly Ala Gly His Leu Phe Ile Ala Leu Asp Val Ala Ala Phe Arg
            265                 270                 275

gat cca caa gat ttc gat gac gca ctc agc gat ctg gtt ggg gaa gtt   979
Asp Pro Gln Asp Phe Asp Asp Ala Leu Ser Asp Leu Val Gly Glu Val
        280                 285                 290

aaa tcc act ccg aaa gca caa aac acc gag gag att ttc tac ccc ggt   1027
Lys Ser Thr Pro Lys Ala Gln Asn Thr Glu Glu Ile Phe Tyr Pro Gly
    295                 300                 305

gaa tcg gaa gac cgt gcg cat cgg aaa aac tct gcg cac ggt att tca   1075
Glu Ser Glu Asp Arg Ala His Arg Lys Asn Ser Ala His Gly Ile Ser
310                 315                 320                 325

ttg cct gaa aaa acg tgg atg gaa ctg caa gaa ctg gca atc gag aac   1123
Leu Pro Glu Lys Thr Trp Met Glu Leu Gln Glu Leu Ala Ile Glu Asn
                330                 335                 340

cat gtt gta act cac cgt tgatctgcgc gttaaacctg gcc                 1164
His Val Val Thr His Arg
            345
```

<210> 20
<211> 347
<212> PRT
<213> Corynebacterium glutamicum

<400> 20

```
Met Pro Glu Val Thr Val Asn Ala Gln Gln Leu Thr Val Leu Cys Thr
 1               5                  10                  15

Asp Ile Leu Thr Lys Thr Gly Val Pro Ala Ala Asp Ala His Leu Val
            20                  25                  30

Gly Asp Ser Leu Val Gln Ala Asp Leu Trp Gly His Pro Ser His Gly
        35                  40                  45

Val Leu Arg Leu Pro Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met
    50                  55                  60

Thr Thr His Ala His Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu
65                  70                  75                  80

Ala Leu Asp Gly His Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala
                85                  90                  95

Arg Lys Glu Ala Val Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val
            100                 105                 110

Ser Val Arg Asn Ser Asn His Phe Gly Thr Ala Met Tyr Tyr Thr Arg
        115                 120                 125

Lys Ala Ala Ala Gln Gly Cys Val Ser Ile Leu Thr Thr Asn Ala Ser
    130                 135                 140

Pro Ala Met Ala Pro Trp Gly Gly Arg Glu Lys Arg Ile Gly Thr Asn
145                 150                 155                 160

Pro Trp Ser Ile Ala Ala Pro Phe Gly Glu Thr Ala Thr Val Val Asp
                165                 170                 175

Ile Ala Asn Thr Ala Val Ala Arg Gly Lys Ile Tyr His Ala Arg Gln
            180                 185                 190

Thr Asn Met Pro Ile Pro Glu Thr Trp Ala Ile Thr Ser Glu Gly Ala
        195                 200                 205

Pro Thr Thr Asp Pro Ala Glu Ala Ile Asn Gly Val Val Leu Pro Met
    210                 215                 220

Ala Gly His Lys Gly Tyr Ala Ile Ser Phe Met Met Asp Val Leu Ser
225                 230                 235                 240

Gly Val Leu Thr Gly Ser Gln His Ser Thr Lys Val His Gly Pro Tyr
                245                 250                 255

Asp Pro Thr Pro Pro Gly Gly Ala Gly His Leu Phe Ile Ala Leu Asp
            260                 265                 270

Val Ala Ala Phe Arg Asp Pro Gln Asp Phe Asp Asp Ala Leu Ser Asp
        275                 280                 285

Leu Val Gly Glu Val Lys Ser Thr Pro Lys Ala Gln Asn Thr Glu Glu
    290                 295                 300

Ile Phe Tyr Pro Gly Glu Ser Glu Asp Arg Ala His Arg Lys Asn Ser
305                 310                 315                 320
```

```
Ala His Gly Ile Ser Leu Pro Glu Lys Thr Trp Met Glu Leu Gln Glu
                325                 330                 335

Leu Ala Ile Glu Asn His Val Val Thr His Arg
            340                 345


<210> 21
<211> 1107
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1084)
<223> RXA01350

<400> 21
tgcagtatcg tcaagatcac ccaaaactgg tggctgttct cttttaagcg ggatagcatg 60

ggttcttaga ggacccccta caaggattga ggattgttta atg aat tcc ccg cag   115
                                          Met Asn Ser Pro Gln
                                            1               5

aac gtc tcc acc aag aag gtc acc gtc acc ggc gca gct ggt caa atc   163
Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly Ala Ala Gly Gln Ile
                10                  15                  20

tct tat tca ctg ttg tgg cgc atc gcc aac ggt gaa gta ttc ggc acc   211
Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly Glu Val Phe Gly Thr
            25                  30                  35

gac acc cct gta gaa ctg aaa ctt ctg gag atc cct cag gct ctt ggc   259
Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile Pro Gln Ala Leu Gly
        40                  45                  50

ggg gca gag ggt gtg gct atg gaa ctt ctg gat tct gcc ttc ccc ctc   307
Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp Ser Ala Phe Pro Leu
    55                  60                  65

ctg cga aac atc acc atc acc gcg gat gcc aat gag gca ttc gac ggc   355
Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn Glu Ala Phe Asp Gly
70                  75                  80                  85

gct aat gcg gcg ttt ttg gtc ggt gcg aag cct cgc gga aaa ggc gaa   403
Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro Arg Gly Lys Gly Glu
                90                  95                  100

gag cgc gca gat ttg ctg gct aac aac ggc aag att ttc gga cct caa   451
Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys Ile Phe Gly Pro Gln
            105                 110                 115

ggt aaa gct atc aat gac aac gcc gca gat gac att cgt gtc cta gtt   499
Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp Ile Arg Val Leu Val
        120                 125                 130

gtt gga aac cca gcg aac acc aac gcg ttg att gct tca gct gcg gcc   547
Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile Ala Ser Ala Ala Ala
    135                 140                 145

cca gat gtt cca gca tcc cgc ttc aac gca atg atg cgc ctt gat cac   595
```

```
Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met Met Arg Leu Asp His
150                 155                 160                 165

aac cgt gcg atc tcc cag ctg gcc acc aag ctt ggc cgt gga tct gcg   643
Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu Gly Arg Gly Ser Ala
                170                 175                 180

gaa ttt aac aac att gtg gtc tgg gga aat cac tcc gca acc cag ttc   691
Glu Phe Asn Asn Ile Val Val Trp Gly Asn His Ser Ala Thr Gln Phe
            185                 190                 195

cca gac atc acc tac gca acc gtt ggt gga gaa aag gtc act gac ctg   739
Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu Lys Val Thr Asp Leu
        200                 205                 210

gtt gat cac gat tgg tat gtg gag gag ttc att cct cgc gtg gct aac   787
Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile Pro Arg Val Ala Asn
    215                 220                 225

cgt ggc gct gaa atc att gag gtc cgt gga aag tct tct gca gct tct   835
Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys Ser Ser Ala Ala Ser
230                 235                 240                 245

gca gca tcc tct gcg att gat cac atg cgc gat tgg gta cag ggc acc   883
Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp Trp Val Gln Gly Thr
                250                 255                 260

gag gcg tgg tcc tct gcg gca att cct tcc acc ggt gca tac ggc att   931
Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr Gly Ala Tyr Gly Ile
            265                 270                 275

cct gag ggc att ttt gtc ggt ctg cca acc gta tcc cgc aac ggt gag   979
Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val Ser Arg Asn Gly Glu
        280                 285                 290

tgg gaa atc gtt gaa ggc ctg gag att tcc gat ttc cag cgc gcc cgc   1027
Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp Phe Gln Arg Ala Arg
    295                 300                 305

atc gac gcg aat gct cag gaa ttg cag gcc gag cgc gag gca gtg cgc   1075
Ile Asp Ala Asn Ala Gln Glu Leu Gln Ala Glu Arg Glu Ala Val Arg
310                 315                 320                 325

gac ttg ctc taatctttaa cgcatgactt cgc                            1107
Asp Leu Leu
```

<210> 22
<211> 328
<212> PRT
<213> Corynebacterium glutamicum

<400> 22

```
Met Asn Ser Pro Gln Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly
  1               5                  10                  15

Ala Ala Gly Gln Ile Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly
            20                  25                  30

Glu Val Phe Gly Thr Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile
```

```
          35                  40                  45

Pro Gln Ala Leu Gly Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp
      50                  55                  60

Ser Ala Phe Pro Leu Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn
 65                  70                  75                  80

Glu Ala Phe Asp Gly Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro
                 85                  90                  95

Arg Gly Lys Gly Glu Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys
            100                 105                 110

Ile Phe Gly Pro Gln Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp
        115                 120                 125

Ile Arg Val Leu Val Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile
    130                 135                 140

Ala Ser Ala Ala Ala Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met
145                 150                 155                 160

Met Arg Leu Asp His Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu
                165                 170                 175

Gly Arg Gly Ser Ala Glu Phe Asn Asn Ile Val Val Trp Gly Asn His
            180                 185                 190

Ser Ala Thr Gln Phe Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu
        195                 200                 205

Lys Val Thr Asp Leu Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile
    210                 215                 220

Pro Arg Val Ala Asn Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys
225                 230                 235                 240

Ser Ser Ala Ala Ser Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp
                245                 250                 255

Trp Val Gln Gly Thr Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr
            260                 265                 270

Gly Ala Tyr Gly Ile Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val
        275                 280                 285

Ser Arg Asn Gly Glu Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp
    290                 295                 300

Phe Gln Arg Ala Arg Ile Asp Ala Asn Ala Gln Glu Leu Gln Ala Glu
305                 310                 315                 320

Arg Glu Ala Val Arg Asp Leu Leu
                325
```

<210> 23
<211> 1092
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1069)
<223> RXA02149

<400> 23
ttgcagagtg aaccacgatg atggttggac agctgttgat agctaatctt tgaaagatta 60

aattcaccta atcctgtgt agaacgcgag gggcactctt atg cca caa aaa ccg 115
Met Pro Gln Lys Pro
1 5

gcc agt ttc gcg gtg ggc ttt gac atc ggc ggc acc aac atg cga gcc 163
Ala Ser Phe Ala Val Gly Phe Asp Ile Gly Gly Thr Asn Met Arg Ala
10 15 20

ggg ctt gtc gac gaa tcc ggg cgc atc gtg acc agt ttg tcg gcg ccg 211
Gly Leu Val Asp Glu Ser Gly Arg Ile Val Thr Ser Leu Ser Ala Pro
25 30 35

tcg ccg cgc acg acg cag gca atg gaa cag ggg att ttt gat cta gtc 259
Ser Pro Arg Thr Thr Gln Ala Met Glu Gln Gly Ile Phe Asp Leu Val
40 45 50

gaa cag ctc aag gcc gaa tac ccg gtt ggt gct gtg gga ctt gcc gtc 307
Glu Gln Leu Lys Ala Glu Tyr Pro Val Gly Ala Val Gly Leu Ala Val
55 60 65

gcg gga ttt ttg gat cct gag tgc gag gtt gtt cga ttt gcc ccg cac 355
Ala Gly Phe Leu Asp Pro Glu Cys Glu Val Val Arg Phe Ala Pro His
70 75 80 85

ctt cct tgg cgc gat gag cca gtg cgt gaa aag ttg gaa aac ctt ttg 403
Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys Leu Glu Asn Leu Leu
90 95 100

ggc ctg cct gtt cgt ttg gaa cat gat gcc aac tca gca gcg tgg ggt 451
Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn Ser Ala Ala Trp Gly
105 110 115

gag cat cgt ttt ggt gca gct caa ggc gct gac aac tgg gtt ttg ttg 499
Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp Asn Trp Val Leu Leu
120 125 130

gca ctc ggc act gga att ggt gca gcg ctg att gaa aaa ggc gaa att 547
Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile Glu Lys Gly Glu Ile
135 140 145

tac cgt ggt gca tat ggc acg gca cca gaa ttt ggt cat ttg cgt gtt 595
Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe Gly His Leu Arg Val
150 155 160 165

gtt cgt ggc gga cgc gca tgt gcg tgt ggc aaa gaa ggc tgc ctg gag 643
Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys Glu Gly Cys Leu Glu
170 175 180

cgt tac tgt tcc ggt act gcc ttg gtt tac act gcg cgt gaa ttg gct 691
Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr Ala Arg Glu Leu Ala
185 190 195

```
tcg cat ggc tca ttc cgc aac agc ggg ctg ttt gac aag atc aaa gcc   739
Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe Asp Lys Ile Lys Ala
        200                 205                 210

gat ccg aat tcc atc aat gga aaa acg atc act gcg gca gcg cgc caa   787
Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr Ala Ala Ala Arg Gln
    215                 220                 225

gaa gac cca ctt gct ctc gcc gtt ctg gaa gat ttc agc gag tgg ctg   835
Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp Phe Ser Glu Trp Leu
230                 235                 240                 245

ggc gaa act ttg gcg atc att gct gat gtc ctt gac cca ggc atg atc   883
Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu Asp Pro Gly Met Ile
                250                 255                 260

atc att ggt ggc gga ctg tcc aat gct gcc gac ctt tat ttg gat cgc   931
Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp Leu Tyr Leu Asp Arg
            265                 270                 275

tcg gtc aac cac tat tcc acc cgc atc gtc ggc gca gga tat cgc cct   979
Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly Ala Gly Tyr Arg Pro
        280                 285                 290

ttg gca cgc gtt gcc aca gct cag ttg ggt gcg gat gct ggc atg atc   1027
Leu Ala Arg Val Ala Thr Ala Gln Leu Gly Ala Asp Ala Gly Met Ile
    295                 300                 305

ggt gtc gct gat cta gct cga cgc tct gta gtg gaa gcc aac           1069
Gly Val Ala Asp Leu Ala Arg Arg Ser Val Val Glu Ala Asn
310                 315                 320

taggtgtttt tcggtgggct gcg                                        1092
```

<210> 24
<211> 323
<212> PRT
<213> Corynebacterium glutamicum

<400> 24

```
Met Pro Gln Lys Pro Ala Ser Phe Ala Val Gly Phe Asp Ile Gly Gly
  1               5                  10                  15

Thr Asn Met Arg Ala Gly Leu Val Asp Glu Ser Gly Arg Ile Val Thr
             20                  25                  30

Ser Leu Ser Ala Pro Ser Pro Arg Thr Thr Gln Ala Met Glu Gln Gly
         35                  40                  45

Ile Phe Asp Leu Val Glu Gln Leu Lys Ala Glu Tyr Pro Val Gly Ala
     50                  55                  60

Val Gly Leu Ala Val Ala Gly Phe Leu Asp Pro Glu Cys Glu Val Val
 65                  70                  75                  80

Arg Phe Ala Pro His Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys
                 85                  90                  95

Leu Glu Asn Leu Leu Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn
            100                 105                 110
```

```
Ser Ala Ala Trp Gly Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp
        115                 120                 125

Asn Trp Val Leu Leu Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile
    130                 135                 140

Glu Lys Gly Glu Ile Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe
145                 150                 155                 160

Gly His Leu Arg Val Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys
                165                 170                 175

Glu Gly Cys Leu Glu Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr
            180                 185                 190

Ala Arg Glu Leu Ala Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe
        195                 200                 205

Asp Lys Ile Lys Ala Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr
    210                 215                 220

Ala Ala Ala Arg Gln Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp
225                 230                 235                 240

Phe Ser Glu Trp Leu Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu
                245                 250                 255

Asp Pro Gly Met Ile Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp
            260                 265                 270

Leu Tyr Leu Asp Arg Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly
        275                 280                 285

Ala Gly Tyr Arg Pro Leu Ala Arg Val Ala Thr Ala Gln Leu Gly Ala
    290                 295                 300

Asp Ala Gly Met Ile Gly Val Ala Asp Leu Ala Arg Arg Ser Val Val
305                 310                 315                 320

Glu Ala Asn
```

<210> 25
<211> 1785
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1762)
<223> RXA01814

<400> 25
tgttaagcca ccctactccg tgaatttgc cgtatctcgt gcgcacaatt gcttttgagg 60

ggaagatgaa gagaaagtat tggtgtttta aggagcaaac atg gca cat gaa cgc 115
                                        Met Ala His Glu Arg
                                          1   5

```
gcc ggg caa ctc gcc caa cca gaa gat ctc atc gat gtt gcg gaa ctg   163
Ala Gly Gln Leu Ala Gln Pro Glu Asp Leu Ile Asp Val Ala Glu Leu
                 10                  15                  20

gtc acc gca tat ttc acc cgc aag ccg gac gtg aac aac cct gat cag   211
Val Thr Ala Tyr Phe Thr Arg Lys Pro Asp Val Asn Asn Pro Asp Gln
             25                  30                  35

cag gtc gct ttc ggc acc tcc gga cac cgt ggc ttc gcg ctg gac agc   259
Gln Val Ala Phe Gly Thr Ser Gly His Arg Gly Phe Ala Leu Asp Ser
         40                  45                  50

gct ttc aac gag gac cac atc ctg gca acc acc cag gcg atc gtc gac   307
Ala Phe Asn Glu Asp His Ile Leu Ala Thr Thr Gln Ala Ile Val Asp
     55                  60                  65

tac cgc aac cag cag cca aaa aac tgg gtc ggc ccg ctg ttt atc ggc   355
Tyr Arg Asn Gln Gln Pro Lys Asn Trp Val Gly Pro Leu Phe Ile Gly
 70                  75                  80                  85

cgc gat acg cac gcg ctg tcc gaa cca gcg atg atc agc gcg ctt gag   403
Arg Asp Thr His Ala Leu Ser Glu Pro Ala Met Ile Ser Ala Leu Glu
                 90                  95                 100

gtc ctc att gcc aac gac gtc gaa gtg ctt gtc gac gcc gac ggc cgc   451
Val Leu Ile Ala Asn Asp Val Glu Val Leu Val Asp Ala Asp Gly Arg
            105                 110                 115

tac acc ccg acg ccc gca gtg tcc cac gcg atc cta cga cac aac gat   499
Tyr Thr Pro Thr Pro Ala Val Ser His Ala Ile Leu Arg His Asn Asp
        120                 125                 130

ggc atc atc ctt ggc acc gca gga ccc tcc cgc ccc tac gcc gac ggc   547
Gly Ile Ile Leu Gly Thr Ala Gly Pro Ser Arg Pro Tyr Ala Asp Gly
    135                 140                 145

atc gtg atc acc cca tcc cac aac cct cct cgt gat ggc gga ttc aaa   595
Ile Val Ile Thr Pro Ser His Asn Pro Pro Arg Asp Gly Gly Phe Lys
150                 155                 160                 165

tac aac cca gcc aac ggt ggc cct gca gat acc gac gcc acc gac tgg   643
Tyr Asn Pro Ala Asn Gly Gly Pro Ala Asp Thr Asp Ala Thr Asp Trp
                170                 175                 180

atc gcc aac cgc gcc aac gat att ctg cgc ggc gac ctt gca gac gtg   691
Ile Ala Asn Arg Ala Asn Asp Ile Leu Arg Gly Asp Leu Ala Asp Val
            185                 190                 195

aag cga gtt cca gtt tcc ggt gtc ctc gac gag cgc acc act gcc tac   739
Lys Arg Val Pro Val Ser Gly Val Leu Asp Glu Arg Thr Thr Ala Tyr
        200                 205                 210

gac ttc aag ggc att tac atc gct gac ctg cca aac gtg gtc aac atc   787
Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro Asn Val Val Asn Ile
    215                 220                 225

gat gcc atc cgc gaa gct ggt gtt cga atc ggc gca gac cca atg ggt   835
Asp Ala Ile Arg Glu Ala Gly Val Arg Ile Gly Ala Asp Pro Met Gly
230                 235                 240                 245

ggc gca tcc gtg gat tac tgg ggt gcc atc gca gaa acc cat ggc ctc   883
```

```
Gly Ala Ser Val Asp Tyr Trp Gly Ala Ile Ala Glu Thr His Gly Leu
                250                 255                 260

aac ctc acc gtg gtc aac cca cac gtt gat tcc acc ttc cgc ttc atg   931
Asn Leu Thr Val Val Asn Pro His Val Asp Ser Thr Phe Arg Phe Met
            265                 270                 275

aca ttg gac acc gac ggc aag atc cgc atg gac tgc tcc agc cca cac   979
Thr Leu Asp Thr Asp Gly Lys Ile Arg Met Asp Cys Ser Ser Pro His
        280                 285                 290

gca atg gca tcg ctg att gac aac cga gac aag ttc gat gtg gca acc   1027
Ala Met Ala Ser Leu Ile Asp Asn Arg Asp Lys Phe Asp Val Ala Thr
    295                 300                 305

ggc aac gac gcc gac gcc gac cgc cac ggc atc gtc acc cca gac gct   1075
Gly Asn Asp Ala Asp Ala Asp Arg His Gly Ile Val Thr Pro Asp Ala
310                 315                 320                 325

ggc ttg atg aac ccc aac cac tac ctc gca gta gca att gag tac ctc   1123
Gly Leu Met Asn Pro Asn His Tyr Leu Ala Val Ala Ile Glu Tyr Leu
                330                 335                 340

ttt gct cac cgc cca ggt tgg tcc gca gat acc gca gtg ggc aaa acc   1171
Phe Ala His Arg Pro Gly Trp Ser Ala Asp Thr Ala Val Gly Lys Thr
            345                 350                 355

ctg gtc agc tcc tcc atg atc gac cgc gtt gtg gcg cag ctt ggc cgc   1219
Leu Val Ser Ser Ser Met Ile Asp Arg Val Val Ala Gln Leu Gly Arg
        360                 365                 370

acc ctc gtt gag gtt cca gtc gga ttc aag tgg ttt gtc cca ggt ttg   1267
Thr Leu Val Glu Val Pro Val Gly Phe Lys Trp Phe Val Pro Gly Leu
    375                 380                 385

atc tcc ggc gaa atc gga ttc ggt ggt gaa gaa tcc gca ggt gca tcc   1315
Ile Ser Gly Glu Ile Gly Phe Gly Gly Glu Glu Ser Ala Gly Ala Ser
390                 395                 400                 405

ttc ctc cgc atg gac ggc acc acc tgg tcc acc gac aag gac ggc ctc   1363
Phe Leu Arg Met Asp Gly Thr Thr Trp Ser Thr Asp Lys Asp Gly Leu
                410                 415                 420

atc ctt gac ctc ctg gca gct gag atc att gca gta acc ggc aag acc   1411
Ile Leu Asp Leu Leu Ala Ala Glu Ile Ile Ala Val Thr Gly Lys Thr
            425                 430                 435

cca tca cag cgc tac gca gaa ctc gcc gaa gaa ttc ggt gca cct gcc   1459
Pro Ser Gln Arg Tyr Ala Glu Leu Ala Glu Glu Phe Gly Ala Pro Ala
        440                 445                 450

tac gcc cgc acc gat gca gaa gcc aac cga gaa caa aag gcc atc ctg   1507
Tyr Ala Arg Thr Asp Ala Glu Ala Asn Arg Glu Gln Lys Ala Ile Leu
    455                 460                 465

aag gca ctg tcc cca gaa cag gtc acc gcc acc gaa cta gcc ggc gaa   1555
Lys Ala Leu Ser Pro Glu Gln Val Thr Ala Thr Glu Leu Ala Gly Glu
470                 475                 480                 485

gca atc acc gct aag ctc acc gaa gct ccc ggc aat ggc gca gcc atc   1603
Ala Ile Thr Ala Lys Leu Thr Glu Ala Pro Gly Asn Gly Ala Ala Ile
```

```
                490                 495                 500

gga gga cta aaa gtg acc acc gaa aac gcc tgg ttc gca gca cgc cca   1651
Gly Gly Leu Lys Val Thr Thr Glu Asn Ala Trp Phe Ala Ala Arg Pro
            505                 510                 515

tcc ggc acc gaa gac aag tac aag atc tac gca gaa tcc ttc aag ggc   1699
Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala Glu Ser Phe Lys Gly
        520                 525                 530

gaa gag cac ctc gcc cag gtt cag aag gaa gcc caa gcg ttg gtc agc   1747
Glu Glu His Leu Ala Gln Val Gln Lys Glu Ala Gln Ala Leu Val Ser
    535                 540                 545

gaa gta ctc gga cag taaaactgcg gacttgctga caa                    1785
Glu Val Leu Gly Gln
550
```

<210> 26
<211> 554
<212> PRT
<213> Corynebacterium glutamicum

<400> 26

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Met Ala His Glu Arg Ala Gly Gln Leu Ala Gln Pro Glu Asp Leu Ile
  1               5                  10                  15

Asp Val Ala Glu Leu Val Thr Ala Tyr Phe Thr Arg Lys Pro Asp Val
             20                  25                  30

Asn Asn Pro Asp Gln Gln Val Ala Phe Gly Thr Ser Gly His Arg Gly
         35                  40                  45

Phe Ala Leu Asp Ser Ala Phe Asn Glu Asp His Ile Leu Ala Thr Thr
     50                  55                  60

Gln Ala Ile Val Asp Tyr Arg Asn Gln Gln Pro Lys Asn Trp Val Gly
 65                  70                  75                  80

Pro Leu Phe Ile Gly Arg Asp Thr His Ala Leu Ser Glu Pro Ala Met
                 85                  90                  95

Ile Ser Ala Leu Glu Val Leu Ile Ala Asn Asp Val Glu Val Leu Val
            100                 105                 110

Asp Ala Asp Gly Arg Tyr Thr Pro Thr Pro Ala Val Ser His Ala Ile
        115                 120                 125

Leu Arg His Asn Asp Gly Ile Ile Leu Gly Thr Ala Gly Pro Ser Arg
    130                 135                 140

Pro Tyr Ala Asp Gly Ile Val Ile Thr Pro Ser His Asn Pro Pro Arg
145                 150                 155                 160

Asp Gly Gly Phe Lys Tyr Asn Pro Ala Asn Gly Gly Pro Ala Asp Thr
                165                 170                 175

Asp Ala Thr Asp Trp Ile Ala Asn Arg Ala Asn Asp Ile Leu Arg Gly
            180                 185                 190
```

Asp Leu Ala Asp Val Lys Arg Val Pro Val Ser Gly Val Leu Asp Glu
195 200 205

Arg Thr Thr Ala Tyr Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro
210 215 220

Asn Val Val Asn Ile Asp Ala Ile Arg Glu Ala Gly Val Arg Ile Gly
225 230 235 240

Ala Asp Pro Met Gly Gly Ala Ser Val Asp Tyr Trp Gly Ala Ile Ala
245 250 255

Glu Thr His Gly Leu Asn Leu Thr Val Val Asn Pro His Val Asp Ser
260 265 270

Thr Phe Arg Phe Met Thr Leu Asp Thr Asp Gly Lys Ile Arg Met Asp
275 280 285

Cys Ser Ser Pro His Ala Met Ala Ser Leu Ile Asp Asn Arg Asp Lys
290 295 300

Phe Asp Val Ala Thr Gly Asn Asp Ala Asp Ala Asp Arg His Gly Ile
305 310 315 320

Val Thr Pro Asp Ala Gly Leu Met Asn Pro Asn His Tyr Leu Ala Val
325 330 335

Ala Ile Glu Tyr Leu Phe Ala His Arg Pro Gly Trp Ser Ala Asp Thr
340 345 350

Ala Val Gly Lys Thr Leu Val Ser Ser Ser Met Ile Asp Arg Val Val
355 360 365

Ala Gln Leu Gly Arg Thr Leu Val Glu Val Pro Val Gly Phe Lys Trp
370 375 380

Phe Val Pro Gly Leu Ile Ser Gly Glu Ile Gly Phe Gly Gly Glu Glu
385 390 395 400

Ser Ala Gly Ala Ser Phe Leu Arg Met Asp Gly Thr Thr Trp Ser Thr
405 410 415

Asp Lys Asp Gly Leu Ile Leu Asp Leu Leu Ala Ala Glu Ile Ile Ala
420 425 430

Val Thr Gly Lys Thr Pro Ser Gln Arg Tyr Ala Glu Leu Ala Glu Glu
435 440 445

Phe Gly Ala Pro Ala Tyr Ala Arg Thr Asp Ala Glu Ala Asn Arg Glu
450 455 460

Gln Lys Ala Ile Leu Lys Ala Leu Ser Pro Glu Gln Val Thr Ala Thr
465 470 475 480

Glu Leu Ala Gly Glu Ala Ile Thr Ala Lys Leu Thr Glu Ala Pro Gly
485 490 495

Asn Gly Ala Ala Ile Gly Gly Leu Lys Val Thr Thr Glu Asn Ala Trp
500 505 510

Phe Ala Ala Arg Pro Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala

515 520 525

Glu Ser Phe Lys Gly Glu Glu His Leu Ala Gln Val Gln Lys Glu Ala
530 535 540

Gln Ala Leu Val Ser Glu Val Leu Gly Gln
545 550

<210> 27
<211> 680
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(657)
<223> RXN02803

<400> 27
gtc tct gga gag atg ctc gcg gca gca ctt tca gca ggc atg gcc agc 48
Val Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser
1 5 10 15

cag ggt gtt gat gtc att cgt gtt ggt gtc atc cca acc cca gct gtt 96
Gln Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val
20 25 30

gca ttc ctc acc gat gat tat ggc gct gac atg ggc gtg atg att tct 144
Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser
35 40 45

gca tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca 192
Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala
50 55 60

ggt gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt 240
Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val
65 70 75 80

atg gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt 288
Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg
85 90 95

gtc atc gaa gaa gca acc gat gca cag gac cgt tac cta gag cac ctg 336
Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu
100 105 110

aag gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat 384
Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp
115 120 125

gca gcc aat ggt gcg gca agt gtt gta gct cca acg gct tat gag gct 432
Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala
130 135 140

gcg ggt gca act gta att gct att cat aac aag cca gac tca tac aac 480
Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn
145 150 155 160

atc aac atg gac tgc ggt tcc acc cac att gat cag gcg cag ccg cca 528

```
Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro
                165                 170                 175

gtc ttg aag cac ggt gct gac ctt gga ctc gcg cat gac ggt gat gct   576
Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala
            180                 185                 190

gac cgt tgt ttg gct gtg aac aag gat gcc aac ctt gtt gat ggt gac   624
Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp
        195                 200                 205

caa atc atg gcg ctg tta gcc att gcg atg aaa taaaacggcg agctgcgcaa 677
Gln Ile Met Ala Leu Leu Ala Ile Ala Met Lys
    210                 215

gaa                                                               680


<210> 28
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 28
Val Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser
  1               5                  10                  15

Gln Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val
            20                  25                  30

Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser
        35                  40                  45

Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala
    50                  55                  60

Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val
65                  70                  75                  80

Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg
                85                  90                  95

Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu
            100                 105                 110

Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp
        115                 120                 125

Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala
    130                 135                 140

Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn
145                 150                 155                 160

Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro
                165                 170                 175

Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala
            180                 185                 190

Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp
```

```
        195                 200                 205

Gln Ile Met Ala Leu Leu Ala Ile Ala Met Lys
    210                 215


<210> 29
<211> 399
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(399)
<223> FRXA02803

<400> 29
tct gga gag atg ctc gcg gca gca ctt tca gca ggc atg gcc agc cag   48
Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser Gln
  1               5                  10                  15

ggt gtt gat gtc att cgt gtt ggt gtc atc cca acc cca gct gtt gca   96
Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val Ala
             20                  25                  30

ttc ctc acc gat gat tat ggc gct gac atg ggc gtg atg att tct gca   144
Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala
         35                  40                  45

tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca ggt   192
Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly
     50                  55                  60

gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt atg   240
Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met
 65                  70                  75                  80

gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt gtc   288
Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val
                 85                  90                  95

atc gaa gaa gca acc gat gca cag gac cgc tac cta gag cac ctg aag   336
Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys
            100                 105                 110

gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat gca   384
Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala
        115                 120                 125

gcc aat ggt gcg gca                                              399
Ala Asn Gly Ala Ala
    130


<210> 30
<211> 133
<212> PRT
<213> Corynebacterium glutamicum

<400> 30
Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser Gln
```

```
  1               5                  10                  15

Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val Ala
            20                  25                  30

Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala
        35                  40                  45

Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly
    50                  55                  60

Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met
65                  70                  75                  80

Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val
                85                  90                  95

Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys
            100                 105                 110

Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala
        115                 120                 125

Ala Asn Gly Ala Ala
    130


<210> 31
<211> 1713
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1690)
<223> RXN03076

<400> 31
aatacctttc tgttttgtcc gcaggcgtat caggaaaacc tgcagcgcgg tagagtcgag 60

tctaatagtg atcccacgaa aacaaaggat cggggtgttc atg gac gag tct cgt   115
                                        Met Asp Glu Ser Arg
                                          1               5

cag ctt agt ttc ggc aca gca ggg ttg cgt gca cca gtt ggc ccg gcg   163
Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala
                10                  15                  20

cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt   211
Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val
            25                  30                  35

gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg   259
Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu
        40                  45                  50

gtt cct gag gat gaa aca gga atc ggc agg gcg ttg tat ccc caa gat   307
Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp
    55                  60                  65

ggt ccg ttg cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tcg cat   355
```

```
Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala Arg Tyr Gly Ser His
 70                  75                  80                  85

act ttt gct gca acc act gcg gag gtg ttc gcg ggt gct ggt ttt gag   403
Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala Gly Ala Gly Phe Glu
                 90                  95                 100

gtg acg ttg ctc ccc acg cct agc cct acg ccg ttg att ccg tgg ttg   451
Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro Leu Ile Pro Trp Leu
            105                 110                 115

gtg aac aag cat ggg ttg gat gcg ggc gtt cag atc acg gct tcg cat   499
Val Asn Lys His Gly Leu Asp Ala Gly Val Gln Ile Thr Ala Ser His
        120                 125                 130

aat ggt gcg gcg gac aat ggc tac aag gtg ttt ttg tct aat ggt cgc   547
Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe Leu Ser Asn Gly Arg
    135                 140                 145

cag ctt tat tct gaa ctg gag cct gag ctt gag gcg cat atc aat gct   595
Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu Ala His Ile Asn Ala
150                 155                 160                 165

gtg gaa gat ccg att cgg gtt cct cgg gtg acg gtg cgc ccc act gct   643
Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr Val Arg Pro Thr Ala
                170                 175                 180

gat cag ctg cgt cga tat gtt gat gag atg gtg tcg ttg gtg act cct   691
Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val Ser Leu Val Thr Pro
            185                 190                 195

gat cag gct gat ttg ttg cgg gtg aat tct gag cgg ggc aat ctt cgc   739
Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu Arg Gly Asn Leu Arg
        200                 205                 210

gtg gtg tat acc gct ctg cat ggt gtg ggt ggc cgc gcg atg gcc aat   787
Val Val Tyr Thr Ala Leu His Gly Val Gly Gly Arg Ala Met Ala Asn
    215                 220                 225

gct ttc caa ttt gct ggt ttt ccc cat act cat ggc gtg aag gct cag   835
Ala Phe Gln Phe Ala Gly Phe Pro His Thr His Gly Val Lys Ala Gln
230                 235                 240                 245

cag tat cct gat ccc acc ttc ccc act gtg gcg ttc ccc aat ccg gaa   883
Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala Phe Pro Asn Pro Glu
                250                 255                 260

gag cct tct gcg att gag ttg ttg ttg gaa cgc gca aag gaa aag aac   931
Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg Ala Lys Glu Lys Asn
            265                 270                 275

gct gac att ttg ttt gcg ctt gat cct gat gcc gat cgt tgt gct gtg   979
Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala Asp Arg Cys Ala Val
        280                 285                 290

ggt att cgt acc gct gat ggc ggc cac cga atg ctc tct ggc gat gag   1027
Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met Leu Ser Gly Asp Glu
    295                 300                 305

gtg ggc aca ctt ttg gct act cgt ttg gtt ccg gag tat tcc ggt gaa   1075
Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro Glu Tyr Ser Gly Glu
```

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310                 315                 320                 325

ggc cca cgt ccc gtg gtt gcc acc acg gtg gtg tct tcg cag ctt ctg   1123
Gly Pro Arg Pro Val Val Ala Thr Thr Val Val Ser Ser Gln Leu Leu
                330                 335                 340

ggt atc atc gcc gag gat aaa ggg tgg gat tat tcc gag aca ctg acg   1171
Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr Ser Glu Thr Leu Thr
            345                 350                 355

gga ttc aaa aat ctg tcg agg gct gcc gat ggt ctc gac gga ccg ctt   1219
Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly Leu Asp Gly Pro Leu
        360                 365                 370

gct ttc gct tat gag gaa gct gtg ggc acc tgc ccg gtt cca gat gtc   1267
Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys Pro Val Pro Asp Val
    375                 380                 385

gtg ccg gat aag gac ggc atc tct aca gcg ttg ttc atg gcg tcg tgg   1315
Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu Phe Met Ala Ser Trp
390                 395                 400                 405

gct gcc gaa ctg aag gct cag ggc gca agc ctg cag caa aaa ctc aat   1363
Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu Gln Gln Lys Leu Asn
                410                 415                 420

gag ttg tat cgc cga tat ggg tat ttt gcg tcc tcg caa att gct gtg   1411
Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser Ser Gln Ile Ala Val
            425                 430                 435

cgc acg agc agt cca cgc gag tta gtt gat cac tgg att gcg cat cct   1459
Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His Trp Ile Ala His Pro
        440                 445                 450

cag caa gaa ctc att gga gtg tct gtc acc cca cat att ctt cct gaa   1507
Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro His Ile Leu Pro Glu
    455                 460                 465

aaa cag ggc att gct ttg cat ggc cag gtg ggg cat gtg cat atc cgt   1555
Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly His Val His Ile Arg
470                 475                 480                 485

gct att ggt cga gtc tct gga act gag gcg aaa gcc aag ctc tat ttg   1603
Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys Ala Lys Leu Tyr Leu
                490                 495                 500

gaa gtt ggt cag gcc agc tcc cat gat gaa gca gct cag ttg ttg cat   1651
Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala Ala Gln Leu Leu His
            505                 510                 515

cag ctg gag gat gaa gtc caa agc tgg ttg agc aag ctt tagtttcctg   1700
Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser Lys Leu
        520                 525                 530

gctgctcccg gtt                                                  1713
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<210> 32
<211> 530
<212> PRT
<213> Corynebacterium glutamicum

<400> 32

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Met Asp Glu Ser Arg Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala
 1               5                  10                  15

Pro Val Gly Pro Ala Arg His Gln Met Asn Val Leu Gln Val Thr Arg
            20                  25                  30

Thr Thr Ala Gly Val Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn
        35                  40                  45

Pro Val Pro His Leu Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala
    50                  55                  60

Leu Tyr Pro Gln Asp Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala
65                  70                  75                  80

Arg Tyr Gly Ser His Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala
                85                  90                  95

Gly Ala Gly Phe Glu Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro
            100                 105                 110

Leu Ile Pro Trp Leu Val Asn Lys His Gly Leu Asp Ala Gly Val Gln
        115                 120                 125

Ile Thr Ala Ser His Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe
    130                 135                 140

Leu Ser Asn Gly Arg Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu
145                 150                 155                 160

Ala His Ile Asn Ala Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr
                165                 170                 175

Val Arg Pro Thr Ala Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val
            180                 185                 190

Ser Leu Val Thr Pro Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu
        195                 200                 205

Arg Gly Asn Leu Arg Val Val Tyr Thr Ala Leu His Gly Val Gly Gly
    210                 215                 220

Arg Ala Met Ala Asn Ala Phe Gln Phe Ala Gly Phe Pro His Thr His
225                 230                 235                 240

Gly Val Lys Ala Gln Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala
                245                 250                 255

Phe Pro Asn Pro Glu Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg
            260                 265                 270

Ala Lys Glu Lys Asn Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala
        275                 280                 285

Asp Arg Cys Ala Val Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met
    290                 295                 300

Leu Ser Gly Asp Glu Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro
305                 310                 315                 320
```

```
Glu Tyr Ser Gly Glu Gly Pro Arg Pro Val Val Ala Thr Thr Val Val
                325                 330                 335

Ser Ser Gln Leu Leu Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr
            340                 345                 350

Ser Glu Thr Leu Thr Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly
        355                 360                 365

Leu Asp Gly Pro Leu Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys
    370                 375                 380

Pro Val Pro Asp Val Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu
385                 390                 395                 400

Phe Met Ala Ser Trp Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu
                405                 410                 415

Gln Gln Lys Leu Asn Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser
            420                 425                 430

Ser Gln Ile Ala Val Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His
        435                 440                 445

Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro
    450                 455                 460

His Ile Leu Pro Glu Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly
465                 470                 475                 480

His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys
                485                 490                 495

Ala Lys Leu Tyr Leu Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala
            500                 505                 510

Ala Gln Leu Leu His Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser
        515                 520                 525

Lys Leu
    530
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<210> 33
<211> 1684
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1684)
<223> FRXA02854

<400> 33
aatacctttc tgttttgtcc gcaggcgtat caggaaaacc tgcagcgcgg tagagtcgag 60

tctaatagtg atcccacgaa aacaaaggat cggggtgttc atg gac gag tct cgt 115
                                    Met Asp Glu Ser Arg
                                      1   5

```
cag ctt agt ttc ggc aca gca ggg ttg cgt gca cca gtt ggc ccg gcg   163
Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala
                 10                  15                  20

cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt   211
Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val
             25                  30                  35

gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg   259
Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu
         40                  45                  50

gtt cct gag gat gaa aca gga atc ggc agg gcg ttg tat ccc caa gat   307
Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp
     55                  60                  65

ggt ccg ttg cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tcg cat   355
Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala Arg Tyr Gly Ser His
 70                  75                  80                  85

act ttt gct gca acc act gcg gag gtg ttc gcg ggt gct ggt ttt gag   403
Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala Gly Ala Gly Phe Glu
                 90                  95                 100

gtg acg ttg ctc ccc acg cct agc cct acg ccg ttg att ccg tgg ttg   451
Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro Leu Ile Pro Trp Leu
             105                 110                 115

gtg aac aag cat ggg ttg gat gcg ggc gtt cag atc acg gct tcg cat   499
Val Asn Lys His Gly Leu Asp Ala Gly Val Gln Ile Thr Ala Ser His
         120                 125                 130

aat ggt gcg gcg gac aat ggc tac aag gtg ttt ttg tct aat ggt cgc   547
Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe Leu Ser Asn Gly Arg
     135                 140                 145

cag ctt tat tct gaa ctg gag cct gag ctt gag gcg cat atc aat gct   595
Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu Ala His Ile Asn Ala
150                 155                 160                 165

gtg gaa gat ccg att cgg gtt cct cgg gtg acg gtg cgc ccc act gct   643
Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr Val Arg Pro Thr Ala
                 170                 175                 180

gat cag ctg cgt cga tat gtt gat gag atg gtg tcg ttg gtg act cct   691
Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val Ser Leu Val Thr Pro
             185                 190                 195

gat cag gct gat ttg ttg cgg gtg aat tct gag cgg ggc aat ctt cgc   739
Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu Arg Gly Asn Leu Arg
         200                 205                 210

gtg gtg tat acc gct ctg cat ggt gtg ggt ggc cgc gcg atg gcc aat   787
Val Val Tyr Thr Ala Leu His Gly Val Gly Gly Arg Ala Met Ala Asn
     215                 220                 225

gct ttc caa ttt gct ggt ttt ccc cat act cat ggc gtg aag gct cag   835
Ala Phe Gln Phe Ala Gly Phe Pro His Thr His Gly Val Lys Ala Gln
230                 235                 240                 245

cag tat cct gat ccc acc ttc ccc act gtg gcg ttc ccc aat ccg gaa   883
```

```
Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala Phe Pro Asn Pro Glu
                250                 255                 260

gag cct tct gcg att gag ttg ttg ttg gaa cgc gca aag gaa aag aac   931
Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg Ala Lys Glu Lys Asn
            265                 270                 275

gct gac att ttg ttt gcg ctt gat cct gat gcc gat cgt tgt gct gtg   979
Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala Asp Arg Cys Ala Val
        280                 285                 290

ggt att cgt acc gct gat ggc ggc cac cga atg ctc tct ggc gat gag   1027
Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met Leu Ser Gly Asp Glu
    295                 300                 305

gtg ggc aca ctt ttg gct act cgt ttg gtt ccg gag tat tcc ggt gaa   1075
Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro Glu Tyr Ser Gly Glu
310                 315                 320                 325

ggc cca cgt ccc gtg gtt gcc acc acg gtg gtg tct tcg cag ctt ctg   1123
Gly Pro Arg Pro Val Val Ala Thr Thr Val Val Ser Ser Gln Leu Leu
                330                 335                 340

ggt atc atc gcc gag gat aaa ggg tgg gat tat tcc gag aca ctg acg   1171
Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr Ser Glu Thr Leu Thr
            345                 350                 355

gga ttc aaa aat ctg tcg agg gct gcc gat ggt ctc gac gga ccg ctt   1219
Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly Leu Asp Gly Pro Leu
        360                 365                 370

gct ttc gct tat gag gaa gct gtg ggc acc tgc ccg gtt cca gat gtc   1267
Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys Pro Val Pro Asp Val
    375                 380                 385

gtg ccg gat aag gac ggc atc tct aca gcg ttg ttc atg gcg tcg tgg   1315
Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu Phe Met Ala Ser Trp
390                 395                 400                 405

gct gcc gaa ctg aag gct cag ggc gca agc ctg cag caa aaa ctc aat   1363
Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu Gln Gln Lys Leu Asn
                410                 415                 420

gag ttg tat cgc cga tat ggg tat ttt gcg tcc tcg caa att gct gtg   1411
Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser Ser Gln Ile Ala Val
            425                 430                 435

cgc acg agc agt cca cgc gag tta gtt gat cac tgg att gcg cat cct   1459
Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His Trp Ile Ala His Pro
        440                 445                 450

cag caa gaa ctc att gga gtg tct gtc acc cca cat att ctt cct gaa   1507
Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro His Ile Leu Pro Glu
    455                 460                 465

aaa cag ggc att gct ttg cat ggc cag gtg ggg cat gtg cat atc cgt   1555
Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly His Val His Ile Arg
470                 475                 480                 485

gct att ggt cga gtc tct gga act gag gcg aaa gcc aag ctc tat ttg   1603
Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys Ala Lys Leu Tyr Leu
```

```
                490                 495                 500

gaa gtt ggt cag gcc agc tcc cat gat gaa gca gct cag ttg ttg cat   1651
Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala Ala Gln Leu Leu His
            505                 510                 515

cag ctg gag gat gaa gtc caa agc tgg ttg agc                       1684
Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser
        520                 525


<210> 34
<211> 528
<212> PRT
<213> Corynebacterium glutamicum

<400> 34
Met Asp Glu Ser Arg Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala
  1               5                  10                  15

Pro Val Gly Pro Ala Arg His Gln Met Asn Val Leu Gln Val Thr Arg
             20                  25                  30

Thr Thr Ala Gly Val Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn
         35                  40                  45

Pro Val Pro His Leu Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala
     50                  55                  60

Leu Tyr Pro Gln Asp Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala
 65                  70                  75                  80

Arg Tyr Gly Ser His Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala
                 85                  90                  95

Gly Ala Gly Phe Glu Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro
            100                 105                 110

Leu Ile Pro Trp Leu Val Asn Lys His Gly Leu Asp Ala Gly Val Gln
        115                 120                 125

Ile Thr Ala Ser His Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe
    130                 135                 140

Leu Ser Asn Gly Arg Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu
145                 150                 155                 160

Ala His Ile Asn Ala Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr
                165                 170                 175

Val Arg Pro Thr Ala Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val
            180                 185                 190

Ser Leu Val Thr Pro Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu
        195                 200                 205

Arg Gly Asn Leu Arg Val Val Tyr Thr Ala Leu His Gly Val Gly Gly
    210                 215                 220

Arg Ala Met Ala Asn Ala Phe Gln Phe Ala Gly Phe Pro His Thr His
225                 230                 235                 240
```

```
Gly Val Lys Ala Gln Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala
                245                 250                 255

Phe Pro Asn Pro Glu Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg
            260                 265                 270

Ala Lys Glu Lys Asn Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala
        275                 280                 285

Asp Arg Cys Ala Val Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met
    290                 295                 300

Leu Ser Gly Asp Glu Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro
305                 310                 315                 320

Glu Tyr Ser Gly Glu Gly Pro Arg Pro Val Val Ala Thr Thr Val Val
                325                 330                 335

Ser Ser Gln Leu Leu Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr
            340                 345                 350

Ser Glu Thr Leu Thr Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly
        355                 360                 365

Leu Asp Gly Pro Leu Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys
    370                 375                 380

Pro Val Pro Asp Val Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu
385                 390                 395                 400

Phe Met Ala Ser Trp Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu
                405                 410                 415

Gln Gln Lys Leu Asn Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser
            420                 425                 430

Ser Gln Ile Ala Val Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His
        435                 440                 445

Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro
    450                 455                 460

His Ile Leu Pro Glu Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly
465                 470                 475                 480

His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys
                485                 490                 495

Ala Lys Leu Tyr Leu Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala
            500                 505                 510

Ala Gln Leu Leu His Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser
        515                 520                 525
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<210> 35
<211> 536

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(513)
<223> RXA00511

<400> 35
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gag ctg cgc aag aac acc ctc gtg ggc act gtc atg agc aac ctg gga   48
Glu Leu Arg Lys Asn Thr Leu Val Gly Thr Val Met Ser Asn Leu Gly
  1               5                  10                  15

ttg aag att gct atg gat gaa gcc gga att aca ctg cgt acc acc aag   96
Leu Lys Ile Ala Met Asp Glu Ala Gly Ile Thr Leu Arg Thr Thr Lys
             20                  25                  30

gta gga gac cgc tac gtg ctg gaa gac ctc aat gca ggt gga ttc agc   144
Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser
         35                  40                  45

ctg ggc ggc gag caa tct ggc cac att gtt ctt cca gat cat ggc acc   192
Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr
     50                  55                  60

act ggc gat gga act ttg act ggt ctt tcc atc atg gcg cgc atg gct   240
Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala
 65                  70                  75                  80

gaa acc gga aag tcc ttg ggc gag ttg gca caa gct atg acg gtg ctg   288
Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu
                 85                  90                  95

cca cag gtt ctg atc aat gtg cca gtt tcg gat aag tcc acc atc gtg   336
Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val
            100                 105                 110

agc cac cca agc gtt gtg gct gcg atc gcg gaa gca gaa gct gag ttg   384
Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu
        115                 120                 125

ggc gcc acc ggt cgc gtt ctt ctt cgt gct tct ggc acc gaa gag ctt   432
Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu
    130                 135                 140

ttc cgc gtg atg gtt gag gct gga gac aag gaa caa gct cgt cgt atc   480
Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile
145                 150                 155                 160

gcg gga cgt ctt gct gca gtg gtt gca gaa gtc taattcactt cagtcacagc 533
Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val
                165                 170

gca                                                               536
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<210> 36
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 36
Glu Leu Arg Lys Asn Thr Leu Val Gly Thr Val Met Ser Asn Leu Gly
1 5 10 15

Leu Lys Ile Ala Met Asp Glu Ala Gly Ile Thr Leu Arg Thr Thr Lys
20 25 30

Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser
35 40 45

Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr
50 55 60

Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala
65 70 75 80

Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu
85 90 95

Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val
100 105 110

Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu
115 120 125

Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu
130 135 140

Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile
145 150 155 160

Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val
165 170

<210> 37
<211> 1497
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1474)
<223> RXN01365

<400> 37
cctgatcagg acgaatcata aggtttgcta ttcggattgg atcctttggc aggggtagga 60

ttgcaagcgt tattttgttc cctaacccct tcgaggattt atg cgt acc cgt gaa 115
Met Arg Thr Arg Glu
1 5

tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt 163
Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
10 15 20

gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt 211
Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
25 30 35

cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac 259

```
Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val Ala Ile Gly His Asp
          40                  45                  50

atg cgt gat tcc tcc cct gaa ttg gcc aag gcg ttt gcc gat ggc gtg   307
Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala Phe Ala Asp Gly Val
     55                  60                  65

act gca cag ggt ttg gat gtt gtt cat ttg gga ctg act tct act gat   355
Thr Ala Gln Gly Leu Asp Val Val His Leu Gly Leu Thr Ser Thr Asp
 70                  75                  80                  85

gag ctg tac ttt gcg tcc gga acc ttg aag tgt gct ggt gcg atg ttt   403
Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys Ala Gly Ala Met Phe
                 90                  95                 100

act gcg tcg cat aac ccc gct gag tac aac ggc atc aag ttg tgt cgt   451
Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly Ile Lys Leu Cys Arg
            105                 110                 115

gcg ggt gct cgt ccg gtc ggt cag gat tct ggt ttg gcc aac atc att   499
Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly Leu Ala Asn Ile Ile
        120                 125                 130

gat gat ctg gtt gag ggt gtt cca gcg ttt gat ggt gag tca ggt tcg   547
Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp Gly Glu Ser Gly Ser
    135                 140                 145

gtt tct gag cag gat ttg ctg agc gca tat gcc gag tac ctc aat gag   595
Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala Glu Tyr Leu Asn Glu
150                 155                 160                 165

ctt gtt gat ctg aag aac atc cgc ccg atg aag gtt gct gtg gat gcg   643
Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys Val Ala Val Asp Ala
                170                 175                 180

gca aac ggc atg ggt ggg ttc act gtc cct gag gta ttc aag ggt ctg   691
Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu Val Phe Lys Gly Leu
            185                 190                 195

cca ctt gat gtt gcg cca ctg tat ttt gag ctt gac ggc aat ttc ccc   739
Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu Asp Gly Asn Phe Pro
        200                 205                 210

aac cat gag gcc aat cct ctg gag cct gcc aac ctg gtt gat ttg cag   787
Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn Leu Val Asp Leu Gln
    215                 220                 225

aag ttt acc gta gag acc gga tct gat atc ggt ttg gcg ttc gac ggc   835
Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly Leu Ala Phe Asp Gly
230                 235                 240                 245

gat gcg gat cgt tgc ttc gtg gtc gat gag aag ggc cag cca gtc agc   883
Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys Gly Gln Pro Val Ser
                250                 255                 260

cct tcg gcg atc tgt gcg atc gta gcg gag cgt tac ttg gag aag ctt   931
Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg Tyr Leu Glu Lys Leu
            265                 270                 275

ccg ggt tcc acc atc atc cac aac ctg att acc tct aag gct gtg cct   979
Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr Ser Lys Ala Val Pro
```

```
        280                 285                 290

gag gtg att gct gaa aac ggt ggc act gcg gtg cgt act cgc gtg ggt   1027
Glu Val Ile Ala Glu Asn Gly Gly Thr Ala Val Arg Thr Arg Val Gly
    295                 300                 305

cac tcc ttc atc aag gcg aag atg gca gag acc ggt gcg gcc ttt ggt   1075
His Ser Phe Ile Lys Ala Lys Met Ala Glu Thr Gly Ala Ala Phe Gly
310                 315                 320                 325

ggc gag cac tct gcg cac tac tac ttc act gag ttc ttc aat gcg gac   1123
Gly Glu His Ser Ala His Tyr Tyr Phe Thr Glu Phe Phe Asn Ala Asp
                330                 335                 340

tcc ggc att ttg gct gcg atg cac gtg ctg gct gcg ctg gga agc cag   1171
Ser Gly Ile Leu Ala Ala Met His Val Leu Ala Ala Leu Gly Ser Gln
            345                 350                 355

gac cag cca ctc agt gag atg atg gct agg tat aac cgg tac gtt gct   1219
Asp Gln Pro Leu Ser Glu Met Met Ala Arg Tyr Asn Arg Tyr Val Ala
        360                 365                 370

tca ggc gag ttg aac tcc cgt ttg gct aat gca gag gcg cag caa gag   1267
Ser Gly Glu Leu Asn Ser Arg Leu Ala Asn Ala Glu Ala Gln Gln Glu
    375                 380                 385

cgc acc cag gct gtg ctc gat gcg ttc gct gat cgc acc gag tcc gtg   1315
Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp Arg Thr Glu Ser Val
390                 395                 400                 405

gac acc ctt gac ggc gtg act gtg gaa ctc aag gac acc tcc gcg tgg   1363
Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys Asp Thr Ser Ala Trp
                410                 415                 420

ttc aac gtg cgt gcg tcc aac acc gag ccg ctg ctt cgc ctc aat gtt   1411
Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu Leu Arg Leu Asn Val
            425                 430                 435

gaa gct gca tcg aag gaa gaa gtc gat gcg ttg gta gcg gag att cta   1459
Glu Ala Ala Ser Lys Glu Glu Val Asp Ala Leu Val Ala Glu Ile Leu
        440                 445                 450

ggg att atc cgc gca taatcccatt ttccggcggg cat                    1497
Gly Ile Ile Arg Ala
    455
```

<210> 38
<211> 458
<212> PRT
<213> Corynebacterium glutamicum

<400> 38

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Met Arg Thr Arg Glu Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val
  1               5                  10                  15

Arg Gly Val Val Gly Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr
             20                  25                  30

Gly Ala Ala Phe Gly Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val
         35                  40                  45
```

```
Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
     50                  55                  60

Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
 65                  70                  75                  80

Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
                 85                  90                  95

Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
            100                 105                 110

Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
        115                 120                 125

Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
    130                 135                 140

Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
145                 150                 155                 160

Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
                165                 170                 175

Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
            180                 185                 190

Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
        195                 200                 205

Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
    210                 215                 220

Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
225                 230                 235                 240

Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
                245                 250                 255

Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
            260                 265                 270

Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr
        275                 280                 285

Ser Lys Ala Val Pro Glu Val Ile Ala Glu Asn Gly Gly Thr Ala Val
    290                 295                 300

Arg Thr Arg Val Gly His Ser Phe Ile Lys Ala Lys Met Ala Glu Thr
305                 310                 315                 320

Gly Ala Ala Phe Gly Gly Glu His Ser Ala His Tyr Tyr Phe Thr Glu
                325                 330                 335

Phe Phe Asn Ala Asp Ser Gly Ile Leu Ala Ala Met His Val Leu Ala
            340                 345                 350

Ala Leu Gly Ser Gln Asp Gln Pro Leu Ser Glu Met Met Ala Arg Tyr
        355                 360                 365
```

```
Asn Arg Tyr Val Ala Ser Gly Glu Leu Asn Ser Arg Leu Ala Asn Ala
    370                 375                 380

Glu Ala Gln Gln Glu Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp
385                 390                 395                 400

Arg Thr Glu Ser Val Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys
                405                 410                 415

Asp Thr Ser Ala Trp Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu
            420                 425                 430

Leu Arg Leu Asn Val Glu Ala Ala Ser Lys Glu Glu Val Asp Ala Leu
        435                 440                 445

Val Ala Glu Ile Leu Gly Ile Ile Arg Ala
    450                 455
```

<210> 39
<211> 994
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(994)
<223> FRXA01365

<400> 39

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cctgatcagg acgaatcata aggtttgcta ttcggattgg atcctttggc aggggtagga 60

ttgcaagcgt tattttgttc cctaacccct tcgaggattt atg cgt acc cgt gaa   115
                                              Met Arg Thr Arg Glu
                                                1               5

tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt   163
Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
                10                  15                  20

gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt   211
Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
            25                  30                  35

cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac   259
Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val Ala Ile Gly His Asp
        40                  45                  50

atg cgt gat tcc tcc cct gaa ttg gcc aag gcg ttt gcc gat ggc gtg   307
Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala Phe Ala Asp Gly Val
    55                  60                  65

act gca cag ggt ttg gat gtt gtt cat ttg gga ctg act tct act gat   355
Thr Ala Gln Gly Leu Asp Val Val His Leu Gly Leu Thr Ser Thr Asp
70                  75                  80                  85

gag ctg tac ttt gcg tcc gga acc ttg aag tgt gct ggt gcg atg ttt   403
Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys Ala Gly Ala Met Phe
                90                  95                  100

act gcg tcg cat aac ccc gct gag tac aac ggc atc aag ttg tgt cgt   451
```

```
Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly Ile Lys Leu Cys Arg
            105                 110                 115

gcg ggt gct cgt ccg gtc ggt cag gat tct ggt ttg gcc aac atc att   499
Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly Leu Ala Asn Ile Ile
        120                 125                 130

gat gat ctg gtt gag ggt gtt cca gcg ttt gat ggt gag tca ggt tcg   547
Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp Gly Glu Ser Gly Ser
    135                 140                 145

gtt tct gag cag gat ttg ctg agc gca tat gcc gag tac ctc aat gag   595
Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala Glu Tyr Leu Asn Glu
150                 155                 160                 165

ctt gtt gat ctg aag aac atc cgc ccg atg aag gtt gct gtg gat gcg   643
Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys Val Ala Val Asp Ala
                170                 175                 180

gca aac ggc atg ggt ggg ttc act gtc cct gag gta ttc aag ggt ctg   691
Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu Val Phe Lys Gly Leu
            185                 190                 195

cca ctt gat gtt gcg cca ctg tat ttt gag ctt gac ggc aat ttc ccc   739
Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu Asp Gly Asn Phe Pro
        200                 205                 210

aac cat gag gcc aat cct ctg gag cct gcc aac ctg gtt gat ttg cag   787
Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn Leu Val Asp Leu Gln
    215                 220                 225

aag ttt acc gta gag acc gga tct gat atc ggt ttg gcg ttc gac ggc   835
Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly Leu Ala Phe Asp Gly
230                 235                 240                 245

gat gcg gat cgt tgc ttc gtg gtc gat gag aag ggc cag cca gtc agc   883
Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys Gly Gln Pro Val Ser
                250                 255                 260

cct tcg gcg atc tgt gcg atc gta gcg gag cgt tac ttg gag aag ctt   931
Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg Tyr Leu Glu Lys Leu
            265                 270                 275

ccg ggt tcc acc atc atc cac aac ctg att acc tct aag gct gtg cct   979
Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr Ser Lys Ala Val Pro
        280                 285                 290

gag gtg att gct gaa                                              994
Glu Val Ile Ala Glu
    295
```

<210> 40
<211> 298
<212> PRT
<213> Corynebacterium glutamicum

<400> 40

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Met Arg Thr Arg Glu Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val
  1               5                  10                  15
```

```
Arg Gly Val Val Gly Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr
            20                  25                  30

Gly Ala Ala Phe Gly Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val
        35                  40                  45

Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
    50                  55                  60

Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
65                  70                  75                  80

Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
                85                  90                  95

Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
            100                 105                 110

Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
        115                 120                 125

Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
    130                 135                 140

Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
145                 150                 155                 160

Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
                165                 170                 175

Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
            180                 185                 190

Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
        195                 200                 205

Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
    210                 215                 220

Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
225                 230                 235                 240

Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
                245                 250                 255

Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
            260                 265                 270

Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr
        275                 280                 285

Ser Lys Ala Val Pro Glu Val Ile Ala Glu
    290                 295
```

<210> 41
<211> 1743
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(1720)
<223> RXA00098

<400> 41
taaatttgtc gtgtttccca ctttgaacac tcttcgatgc gcttggccac aaaagcaagc 60

taacctgaag atgttattta acgacaataa aggagttttc atg gcg gac att tcg 115
Met Ala Asp Ile Ser
1 5

acc acc cag gtt tgg caa gac ctg acc gat cat tac tca aac ttc cag 163
Thr Thr Gln Val Trp Gln Asp Leu Thr Asp His Tyr Ser Asn Phe Gln
10 15 20

gca acc act ctg cgt gaa ctt ttc aag gaa gaa aac cgc gcc gag aag 211
Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu Asn Arg Ala Glu Lys
25 30 35

tac acc ttc tcc gcg gct ggc ctc cac gtc gac ctg tcg aag aat ctg 259
Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp Leu Ser Lys Asn Leu
40 45 50

ctt gac gac gcc acc ctc acc aag ctc ctt gca ctg acc gaa gaa tct 307
Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala Leu Thr Glu Glu Ser
55 60 65

ggc ctt cgc gaa cgc att gac gcg atg ttt gcc ggt gaa cac ctc aac 355
Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala Gly Glu His Leu Asn
70 75 80 85

aac acc gaa gac cgc gct gtc ctc cac acc gcg ctg cgc ctt cct gcc 403
Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala Leu Arg Leu Pro Ala
90 95 100

gaa gct gat ctg tca gta gat ggc caa gat gtt gct gct gat gtc cac 451
Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val Ala Ala Asp Val His
105 110 115

gaa gtt ttg gga cgc atg cgt gac ttc gct act gcg ctg cgc tca ggc 499
Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr Ala Leu Arg Ser Gly
120 125 130

aac tgg ttg gga cac acc ggc cac acg atc aag aag atc gtc aac att 547
Asn Trp Leu Gly His Thr Gly His Thr Ile Lys Lys Ile Val Asn Ile
135 140 145

ggt atc ggt ggc tct gac ctc gga cca gcc atg gct acg aag gct ctg 595
Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met Ala Thr Lys Ala Leu
150 155 160 165

cgt gca tac gcg acc gct ggt atc tca gca gaa ttc gtc tcc aac gtc 643
Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu Phe Val Ser Asn Val
170 175 180

gac cca gca gac ctc gtt tct gtg ttg gaa gac ctc gat gca gaa tcc 691
Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp Leu Asp Ala Glu Ser
185 190 195

aca ttg ttc gtg atc gct tcg aaa act ttc acc acc cag gag acg ctg 739
Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr Thr Gln Glu Thr Leu

```
        200                 205                 210

tcc aac gct cgt gca gct cgt gct tgg ctg gta gag aag ctc ggt gaa   787
Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val Glu Lys Leu Gly Glu
    215                 220                 225

gag gct gtc gcg aag cac ttc gtc gca gtg tcc acc aat gct gaa aag   835
Glu Ala Val Ala Lys His Phe Val Ala Val Ser Thr Asn Ala Glu Lys
230                 235                 240                 245

gtc gca gag ttc ggt atc gac acg gac aac atg ttc ggc ttc tgg gac   883
Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met Phe Gly Phe Trp Asp
                250                 255                 260

tgg gtc gga ggt cgt tac tcc gtg gac tcc gca gtt ggt ctt tcc ctc   931
Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala Val Gly Leu Ser Leu
            265                 270                 275

atg gca gtg atc ggc cct cgc gac ttc atg cgt ttc ctc ggt gga ttc   979
Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg Phe Leu Gly Gly Phe
        280                 285                 290

cac gcg atg gat gaa cac ttc cgc acc acc aag ttc gaa gag aac gtt   1027
His Ala Met Asp Glu His Phe Arg Thr Thr Lys Phe Glu Glu Asn Val
    295                 300                 305

cca atc ttg atg gct ctg ctc ggt gtc tgg tac tcc gat ttc tat ggt   1075
Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr Ser Asp Phe Tyr Gly
310                 315                 320                 325

gca gaa acc cac gct gtc cta cct tat tcc gag gat ctc agc cgt ttt   1123
Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu Asp Leu Ser Arg Phe
                330                 335                 340

gct gct tac ctc cag cag ctg acc atg gaa tca aat ggc aag tca gtc   1171
Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser Asn Gly Lys Ser Val
            345                 350                 355

cac cgc gac ggc tcc cct gtt tcc act ggc act ggc gaa att tac tgg   1219
His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr Gly Glu Ile Tyr Trp
        360                 365                 370

ggt gag cct ggc aca aat ggc cag cac gct ttc ttc cag ctg atc cac   1267
Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe Phe Gln Leu Ile His
    375                 380                 385

cag ggc act cgc ctt gtt cca gct gat ttc att ggt ttc gct cgt cca   1315
Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile Gly Phe Ala Arg Pro
390                 395                 400                 405

aag cag gat ctt cct gcc ggt gag cgc acc atg cat gac ctt ttg atg   1363
Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met His Asp Leu Leu Met
                410                 415                 420

agc aac ttc ttc gca cag acc aag gtt ttg gct ttc ggt aag aac gct   1411
Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala Phe Gly Lys Asn Ala
            425                 430                 435

gaa gag atc gct gcg gaa ggt gtc gca cct gag ctg gtc aac cac aag   1459
Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu Leu Val Asn His Lys
        440                 445                 450
```

```
gtc atg cca ggt aat cgc cca acc acc acc att ttg gcg gag gaa ctt   1507
Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile Leu Ala Glu Glu Leu
    455                 460                 465

acc cct tct att ctc ggt gcg ttg atc gct ttg tac gaa cac atc gtg   1555
Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Ile Val
470                 475                 480                 485

atg gtt cag ggc gtg att tgg gac atc aac tcc ttc gac caa tgg ggt   1603
Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser Phe Asp Gln Trp Gly
                490                 495                 500

gtt gaa ctg ggc aaa cag cag gca aat gac ctc gct ccg gct gtc tct   1651
Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu Ala Pro Ala Val Ser
            505                 510                 515

ggt gaa gag gat gtt gac tcg gga gat tct tcc act gat tca ctg att   1699
Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser Thr Asp Ser Leu Ile
        520                 525                 530

aag tgg tac cgc gca aat agg tagtcgcttg cttatagggt cag            1743
Lys Trp Tyr Arg Ala Asn Arg
    535                 540
```

<210> 42
<211> 540
<212> PRT
<213> Corynebacterium glutamicum

<400> 42

```
Met Ala Asp Ile Ser Thr Thr Gln Val Trp Gln Asp Leu Thr Asp His
  1               5                  10                  15

Tyr Ser Asn Phe Gln Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu
             20                  25                  30

Asn Arg Ala Glu Lys Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp
         35                  40                  45

Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala
     50                  55                  60

Leu Thr Glu Glu Ser Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala
 65                  70                  75                  80

Gly Glu His Leu Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala
                 85                  90                  95

Leu Arg Leu Pro Ala Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val
            100                 105                 110

Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr
        115                 120                 125

Ala Leu Arg Ser Gly Asn Trp Leu Gly His Thr Gly His Thr Ile Lys
    130                 135                 140

Lys Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met
145                 150                 155                 160
```

```
Ala Thr Lys Ala Leu Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu
                165                 170                 175

Phe Val Ser Asn Val Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp
            180                 185                 190

Leu Asp Ala Glu Ser Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr
        195                 200                 205

Thr Gln Glu Thr Leu Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val
    210                 215                 220

Glu Lys Leu Gly Glu Glu Ala Val Ala Lys His Phe Val Ala Val Ser
225                 230                 235                 240

Thr Asn Ala Glu Lys Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met
                245                 250                 255

Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala
            260                 265                 270

Val Gly Leu Ser Leu Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg
        275                 280                 285

Phe Leu Gly Gly Phe His Ala Met Asp Glu His Phe Arg Thr Thr Lys
    290                 295                 300

Phe Glu Glu Asn Val Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr
305                 310                 315                 320

Ser Asp Phe Tyr Gly Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu
                325                 330                 335

Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser
            340                 345                 350

Asn Gly Lys Ser Val His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr
        355                 360                 365

Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe
    370                 375                 380

Phe Gln Leu Ile His Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile
385                 390                 395                 400

Gly Phe Ala Arg Pro Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met
                405                 410                 415

His Asp Leu Leu Met Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala
            420                 425                 430

Phe Gly Lys Asn Ala Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu
        435                 440                 445

Leu Val Asn His Lys Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile
    450                 455                 460

Leu Ala Glu Glu Leu Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu
465                 470                 475                 480
```

```
Tyr Glu His Ile Val Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser
                485                 490                 495

Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu
            500                 505                 510

Ala Pro Ala Val Ser Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser
        515                 520                 525

Thr Asp Ser Leu Ile Lys Trp Tyr Arg Ala Asn Arg
    530                 535                 540


<210> 43
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(630)
<223> RXA01989

<400> 43
gtt aaa tca att cac aaa aca att cat gaa ggt act ggt gca ggt agt   48
Val Lys Ser Ile His Lys Thr Ile His Glu Gly Thr Gly Ala Gly Ser
  1               5                  10                  15

gac ttc tta ggc tgg gtt gat tta cca gtt gat tac gac aaa gaa gaa   96
Asp Phe Leu Gly Trp Val Asp Leu Pro Val Asp Tyr Asp Lys Glu Glu
            20                  25                  30

ttt tca aga att gtt gaa gca tca aaa cgc att aaa gaa aat tct gat   144
Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp
        35                  40                  45

gtt tta gta gtc atc ggt att ggt ggt tct tac tta ggt gca cgt gca   192
Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala
    50                  55                  60

gca atc gaa atg tta acg tca tca ttt aga aac agc aat gaa tac cct   240
Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro
65                  70                  75                  80

gaa att gta ttt gtt ggt aat cac tta tca tca aca tat acg aaa gag   288
Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu
                85                  90                  95

tta gtt gat tat tta gca gac aaa gat ttc tct gta aac gtt att tct   336
Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser
            100                 105                 110

aaa tct ggt aca act aca gaa cca gca gtt gca ttt aga ttg ttc aaa   384
Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys
        115                 120                 125

caa tta gtt gaa gaa aga tac ggt aaa gaa gaa gca caa aaa cgt ata   432
Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile
    130                 135                 140

ttt gca aca acg gat aaa gaa aaa ggt gct tta aaa cag ttg gct aca   480
```

```
Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr
145                 150                 155                 160

aac gaa ggt tat gaa acg ttt atc gta cct gat gat gta ggt gga aga   528
Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg
                165                 170                 175

tat tct gtt tta aca gca gta gga tta tta cca att gca aca gct gga   576
Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly
            180                 185                 190

att aac atc gaa gct atg atg att ggt gct gca aaa gca cgt gaa gaa   624
Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu
        195                 200                 205

tta tct                                                          630
Leu Ser
    210
```

<210> 44
<211> 210
<212> PRT
<213> Corynebacterium glutamicum

<400> 44

```
Val Lys Ser Ile His Lys Thr Ile His Glu Gly Thr Gly Ala Gly Ser
  1               5                  10                  15

Asp Phe Leu Gly Trp Val Asp Leu Pro Val Asp Tyr Asp Lys Glu Glu
             20                  25                  30

Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp
         35                  40                  45

Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala
     50                  55                  60

Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro
 65                  70                  75                  80

Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu
                 85                  90                  95

Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser
            100                 105                 110

Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys
        115                 120                 125

Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile
    130                 135                 140

Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr
145                 150                 155                 160

Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg
                165                 170                 175

Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly
            180                 185                 190
```

```
Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu
        195                 200                 205

Leu Ser
    210


<210> 45
<211> 1269
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1246)
<223> RXA00340

<400> 45
cggtatctcc gacatccgca acacccccaa agatgaggtt ccacagtgcc cagaatgtgg 60

ctcttacctc atcactgaca tctcttagaa agaccaccca gtg aaa tta gtc atc   115
                                            Val Lys Leu Val Ile
                                              1               5

gag gcc gac ggc ggc tcc cgc gga aac ccc ggc gtc gcc ggc tcc ggc   163
Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly Val Ala Gly Ser Gly
                10                  15                  20

acc gtg gtg tac tcc gac aac aaa gca gaa gtt ctc aaa gaa atc gcc   211
Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val Leu Lys Glu Ile Ala
            25                  30                  35

tat gtt gtc gga aca aaa gcc acc aac aac gtc gcc gaa tac cgc gga   259
Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val Ala Glu Tyr Arg Gly
        40                  45                  50

cta ctc gaa ggc ctc aaa gca gcc cgc gag ctc ggc gct acc tcc gtg   307
Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu Gly Ala Thr Ser Val
    55                  60                  65

gat gtc tac atg gac tcc aaa ctt gtc gtt gaa caa atg tcc ggc cgg   355
Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu Gln Met Ser Gly Arg
70                  75                  80                  85

tgg aaa atc aaa cac ccc gac atg aaa gtt cta gcg atc gaa gcc aag   403
Trp Lys Ile Lys His Pro Asp Met Lys Val Leu Ala Ile Glu Ala Lys
                90                  95                  100

gag att gct tcc gaa atc ggg tcc gtt tct tat acg tgg att ccg cgt   451
Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr Thr Trp Ile Pro Arg
            105                 110                 115

gag aaa aac aaa cga gct gac gca ttg tcc aac gtg gcg atg gat gct   499
Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn Val Ala Met Asp Ala
        120                 125                 130

gca gcg gca ggt aag ccg gta ggt gtt gta ggg gat tct gct tct gta   547
Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly Asp Ser Ala Ser Val
    135                 140                 145
```

```
tct tct gct tct tcg gtt gcg ggc tca gag aaa gaa gac ctc aac tgc   595
Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys Glu Asp Leu Asn Cys
150                 155                 160                 165

acc gaa acc aaa ccc acc aac tgg aac ggc gca acc aca gat ccc act   643
Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala Thr Thr Asp Pro Thr
                170                 175                 180

cgt ttc ttg ttg ctt cgc cac ggc caa act gct atg tca gtg gca cgc   691
Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala Met Ser Val Ala Arg
            185                 190                 195

ctt tac tcc ggt agg tcc aac cca gag ctg tct gaa ctt ggt gaa aaa   739
Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser Glu Leu Gly Glu Lys
        200                 205                 210

caa gca gca gcg gca gca cga cga ctc gct caa acc ggt ggc atc gac   787
Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln Thr Gly Gly Ile Asp
    215                 220                 225

gct att gtg agt tct ccg ctc acc cgc acg atg caa acc gca gaa gca   835
Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met Gln Thr Ala Glu Ala
230                 235                 240                 245

gca gcg gcc gca ctg gga atg aaa gta cgt gtt atc gat gat ctc atc   883
Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val Ile Asp Asp Leu Ile
                250                 255                 260

gaa act gac ttt gga ctg tgg gat gga aaa tca ttt tca gaa gcc cac   931
Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser Phe Ser Glu Ala His
            265                 270                 275

gaa caa gat cca gaa ctg cac acc aag tgg ctc act gac tca tct gta   979
Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu Thr Asp Ser Ser Val
        280                 285                 290

gcc cca ccc ggt ggt gag tcc ctg cag acg gtt aat cga cgt gtg aaa   1027
Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val Asn Arg Arg Val Lys
    295                 300                 305

aag gct cgt gaa agc ctc caa cgc gaa tac ggt gca gcg aat gtt ttg   1075
Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly Ala Ala Asn Val Leu
310                 315                 320                 325

gtg gtc agc cac gtc acc cca atc aaa gcc atc atg agg caa gca ttg   1123
Val Val Ser His Val Thr Pro Ile Lys Ala Ile Met Arg Gln Ala Leu
                330                 335                 340

gac gca ggc cca tcc ttc ttt cag aag gca cac ctt gac ttg gcg tcg   1171
Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His Leu Asp Leu Ala Ser
            345                 350                 355

ctg tcg atc gca gag ttt tac gaa gac ggc cca acc tgc gta aga ctg   1219
Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro Thr Cys Val Arg Leu
        360                 365                 370

ttc aac gac acc tca cac ctg gaa gcg tgacgacagt ctgacggaag        1266
Phe Asn Asp Thr Ser His Leu Glu Ala
    375                 380

ctc                                                              1269
```

<210> 46
<211> 382
<212> PRT
<213> Corynebacterium glutamicum

<400> 46

```
Val Lys Leu Val Ile Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly
  1               5                  10                  15

Val Ala Gly Ser Gly Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val
             20                  25                  30

Leu Lys Glu Ile Ala Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val
         35                  40                  45

Ala Glu Tyr Arg Gly Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu
     50                  55                  60

Gly Ala Thr Ser Val Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu
 65                  70                  75                  80

Gln Met Ser Gly Arg Trp Lys Ile Lys His Pro Asp Met Lys Val Leu
                 85                  90                  95

Ala Ile Glu Ala Lys Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr
            100                 105                 110

Thr Trp Ile Pro Arg Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn
        115                 120                 125

Val Ala Met Asp Ala Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly
    130                 135                 140

Asp Ser Ala Ser Val Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys
145                 150                 155                 160

Glu Asp Leu Asn Cys Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala
                165                 170                 175

Thr Thr Asp Pro Thr Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala
            180                 185                 190

Met Ser Val Ala Arg Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser
        195                 200                 205

Glu Leu Gly Glu Lys Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln
    210                 215                 220

Thr Gly Gly Ile Asp Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met
225                 230                 235                 240

Gln Thr Ala Glu Ala Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val
                245                 250                 255

Ile Asp Asp Leu Ile Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser
            260                 265                 270

Phe Ser Glu Ala His Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu
        275                 280                 285
```

```
Thr Asp Ser Ser Val Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val
    290                 295                 300

Asn Arg Arg Val Lys Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly
305                 310                 315                 320

Ala Ala Asn Val Leu Val Val Ser His Val Thr Pro Ile Lys Ala Ile
                325                 330                 335

Met Arg Gln Ala Leu Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His
            340                 345                 350

Leu Asp Leu Ala Ser Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro
        355                 360                 365

Thr Cys Val Arg Leu Phe Asn Asp Thr Ser His Leu Glu Ala
    370                 375                 380


<210> 47
<211> 840
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(817)
<223> RXA02492

<400> 47
gctgtacaac gacgctattg ccaacgaaaa tgtcgacggt gaaacgcatc acggctaagt 60

aaacgcgcgt cgtggaacat aaagtggcaa actagtacct atg act aac gga aaa   115
                                        Met Thr Asn Gly Lys
                                          1               5

ttg att ctt ctt cgt cac ggt cag agc gaa tgg aac gca tcc aac cag   163
Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp Asn Ala Ser Asn Gln
                10                  15                  20

ttc act gga tgg gtc gac gtc aat ctg acc gaa cag ggt gag gct gag   211
Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu Gln Gly Glu Ala Glu
            25                  30                  35

gcc aaa ggc gtc ctc cca ggc gtt gta tac acc tcc ttg ctg cgt cgc   259
Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr Ser Leu Leu Arg Arg
        40                  45                  50

gcg atc cgc act gca aac atc gca ctg aac gct gca gac cgc cac tgg   307
Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala Ala Asp Arg His Trp
    55                  60                  65

atc cca gtg atc cgc gac tgg cgc ctc aac gag cgt cac tac ggc gca   355
Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala
70                  75                  80                  85

ctg cag ggc ctt gac aag gct gca acc aag gaa aaa tac ggc gac gac   403
Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu Lys Tyr Gly Asp Asp
                90                  95                  100
```

```
cag ttc atg gaa tgg cgc cgc tcc tac gac acc cca cca cca gag ctc   451
Gln Phe Met Glu Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Glu Leu
            105                 110                 115

gcg gat gac gca gag tac tcc cag gca aat gac cct cgt tac gcg gac   499
Ala Asp Asp Ala Glu Tyr Ser Gln Ala Asn Asp Pro Arg Tyr Ala Asp
        120                 125                 130

ctc gac gta gtt cca cgc acc gaa tgc ctc aag gac gtt gtg gtt cgt   547
Leu Asp Val Val Pro Arg Thr Glu Cys Leu Lys Asp Val Val Val Arg
    135                 140                 145

ttt gtt cct tac ttc gag gaa gaa atc ctg cca cgc gca aag aag ggc   595
Phe Val Pro Tyr Phe Glu Glu Glu Ile Leu Pro Arg Ala Lys Lys Gly
150                 155                 160                 165

gaa acc gtc ctc atc gca gca cac ggc aac tcc ctg cgt gcg ctg gtt   643
Glu Thr Val Leu Ile Ala Ala His Gly Asn Ser Leu Arg Ala Leu Val
                170                 175                 180

aag cac ctt gac ggc atc tcc gat gct gat atc gca gag ctc aac atc   691
Lys His Leu Asp Gly Ile Ser Asp Ala Asp Ile Ala Glu Leu Asn Ile
            185                 190                 195

cca acc ggc atc cca ctg gtc tac gaa atc gcc gaa gac ggt tcc gta   739
Pro Thr Gly Ile Pro Leu Val Tyr Glu Ile Ala Glu Asp Gly Ser Val
        200                 205                 210

gta aac cca ggc ggc acc tac ctc gat cct gag gca gca gca gcc ggc   787
Val Asn Pro Gly Gly Thr Tyr Leu Asp Pro Glu Ala Ala Ala Ala Gly
    215                 220                 225

gca gca gca gta gca aac cag ggt aat aag tagctatttg taggtgagca     837
Ala Ala Ala Val Ala Asn Gln Gly Asn Lys
230                 235

ctc                                                               840
```

<210> 48
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 48

```
Met Thr Asn Gly Lys Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp
  1               5                  10                  15

Asn Ala Ser Asn Gln Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu
             20                  25                  30

Gln Gly Glu Ala Glu Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr
         35                  40                  45

Ser Leu Leu Arg Arg Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala
     50                  55                  60

Ala Asp Arg His Trp Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu
 65                  70                  75                  80

Arg His Tyr Gly Ala Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu
```

```
                85                  90                  95

Lys Tyr Gly Asp Asp Gln Phe Met Glu Trp Arg Arg Ser Tyr Asp Thr
            100                 105                 110

Pro Pro Pro Glu Leu Ala Asp Asp Ala Glu Tyr Ser Gln Ala Asn Asp
        115                 120                 125

Pro Arg Tyr Ala Asp Leu Asp Val Val Pro Arg Thr Glu Cys Leu Lys
    130                 135                 140

Asp Val Val Val Arg Phe Val Pro Tyr Phe Glu Glu Glu Ile Leu Pro
145                 150                 155                 160

Arg Ala Lys Lys Gly Glu Thr Val Leu Ile Ala Ala His Gly Asn Ser
                165                 170                 175

Leu Arg Ala Leu Val Lys His Leu Asp Gly Ile Ser Asp Ala Asp Ile
            180                 185                 190

Ala Glu Leu Asn Ile Pro Thr Gly Ile Pro Leu Val Tyr Glu Ile Ala
        195                 200                 205

Glu Asp Gly Ser Val Val Asn Pro Gly Gly Thr Tyr Leu Asp Pro Glu
    210                 215                 220

Ala Ala Ala Ala Gly Ala Ala Ala Val Ala Asn Gln Gly Asn Lys
225                 230                 235


<210> 49
<211> 729
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(706)
<223> RXA00381

<400> 49
aaacctggtt tgtgtcttcc gctctcacgg acgatgattt ctccaagatc gagcaggcac 60

tcaagcccgc cgcacgtgca gcagcagaag cgaaggcatc atg acg caa acc att   115
                                            Met Thr Gln Thr Ile
                                              1               5

gtc cat cta gtt cgc cac ggc gaa gtc cac aac cca gag aaa atc ctg   163
Val His Leu Val Arg His Gly Glu Val His Asn Pro Glu Lys Ile Leu
                  10                  15                  20

tac gga cgc atg ccc gga tac agg ttg tct tcc cgt gga cgc agc caa   211
Tyr Gly Arg Met Pro Gly Tyr Arg Leu Ser Ser Arg Gly Arg Ser Gln
              25                  30                  35

gcc gcc cgc act gca gct tct ttt gaa ggc cac gat gtc acc tac att   259
Ala Ala Arg Thr Ala Ala Ser Phe Glu Gly His Asp Val Thr Tyr Ile
          40                  45                  50

gcg gcc tcc cca ttg cag cgt gtg cag gaa acc tcc gaa ccg ttc atc   307
Ala Ala Ser Pro Leu Gln Arg Val Gln Glu Thr Ser Glu Pro Phe Ile
```

```
      55                  60                  65

aag gtc aca ggc cta gaa ctg atc acc gac gag gat ctt ctg gaa gca   355
Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu Asp Leu Leu Glu Ala
 70                  75                  80                  85

ggc aac cgt ttc gaa ggc ctg cgc acc aaa ggt tgg cgt tcc cag ttg   403
Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly Trp Arg Ser Gln Leu
                 90                  95                 100

tgg aac ccc gtg cgt tgg cct ttg atg tac aac ccc acg ctt ccc agc   451
Trp Asn Pro Val Arg Trp Pro Leu Met Tyr Asn Pro Thr Leu Pro Ser
            105                 110                 115

tgg ggc gaa cac tac acc gac att ttg gaa aga atg atg gcg gct gtg   499
Trp Gly Glu His Tyr Thr Asp Ile Leu Glu Arg Met Met Ala Ala Val
        120                 125                 130

gaa cga gct cgg gtg gca gcg gaa gga cac gaa gca atc ctg gtg acc   547
Glu Arg Ala Arg Val Ala Ala Glu Gly His Glu Ala Ile Leu Val Thr
    135                 140                 145

cac cag ttg ccg atc gtg tgc gtg caa cgc cac gcc cgc gga caa agc   595
His Gln Leu Pro Ile Val Cys Val Gln Arg His Ala Arg Gly Gln Ser
150                 155                 160                 165

ctg tcc cat aac cca gcg acc agg caa tgc gac ctc gcc tca gtg aca   643
Leu Ser His Asn Pro Ala Thr Arg Gln Cys Asp Leu Ala Ser Val Thr
                170                 175                 180

tcc ttg gtg ttc caa gac gat caa att gtc ggc gtg cat tac aac gaa   691
Ser Leu Val Phe Gln Asp Asp Gln Ile Val Gly Val His Tyr Asn Glu
            185                 190                 195

cca gct cag gag att tgatcactcg tgcgtttgac caa                    729
Pro Ala Gln Glu Ile
        200
```

<210> 50
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 50

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Met Thr Gln Thr Ile Val His Leu Val Arg His Gly Glu Val His Asn
  1               5                  10                  15

Pro Glu Lys Ile Leu Tyr Gly Arg Met Pro Gly Tyr Arg Leu Ser Ser
             20                  25                  30

Arg Gly Arg Ser Gln Ala Ala Arg Thr Ala Ala Ser Phe Glu Gly His
         35                  40                  45

Asp Val Thr Tyr Ile Ala Ala Ser Pro Leu Gln Arg Val Gln Glu Thr
     50                  55                  60

Ser Glu Pro Phe Ile Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu
 65                  70                  75                  80

Asp Leu Leu Glu Ala Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly
```

```
                85                  90                  95

Trp Arg Ser Gln Leu Trp Asn Pro Val Arg Trp Pro Leu Met Tyr Asn
            100                 105                 110

Pro Thr Leu Pro Ser Trp Gly Glu His Tyr Thr Asp Ile Leu Glu Arg
        115                 120                 125

Met Met Ala Ala Val Glu Arg Ala Arg Val Ala Ala Glu Gly His Glu
    130                 135                 140

Ala Ile Leu Val Thr His Gln Leu Pro Ile Val Cys Val Gln Arg His
145                 150                 155                 160

Ala Arg Gly Gln Ser Leu Ser His Asn Pro Ala Thr Arg Gln Cys Asp
                165                 170                 175

Leu Ala Ser Val Thr Ser Leu Val Phe Gln Asp Asp Gln Ile Val Gly
            180                 185                 190

Val His Tyr Asn Glu Pro Ala Gln Glu Ile
        195                 200
```

<210> 51
<211> 822
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(799)
<223> RXA02122

<400> 51

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ggccttcagc tcaccgacag tttgtacatt tggtggaaga ctcacacccc acaccctaga 60

ccttttttta agtgggcggt caggaatttt tcgcacaggt atg ctg cat gtc atg   115
                                              Met Leu His Val Met
                                                1               5

aag ccg ggt tca cac gca gct gcc gaa aag act caa tcc act gtg gtt   163
Lys Pro Gly Ser His Ala Ala Ala Glu Lys Thr Gln Ser Thr Val Val
                10                  15                  20

tta ctc att cgg cat ggg caa acc cca aca act ggt cag gtt ctg cct   211
Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr Gly Gln Val Leu Pro
            25                  30                  35

ggt cag acg ccg ggt tta cac ctg tct gat aag ggt gaa gag cag gcg   259
Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys Gly Glu Glu Gln Ala
        40                  45                  50

cgg gag gtg gca cag cgt ctg gcg gag gtg ccg att acc gct gtg tat   307
Arg Glu Val Ala Gln Arg Leu Ala Glu Val Pro Ile Thr Ala Val Tyr
    55                  60                  65

tca tcg ccg atg gag cgt gcg cag gaa aca gca gca ccg acg gtc agc   355
Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala Ala Pro Thr Val Ser
70                  75                  80                  85
```

```
gct cat ggc ctc gag ttg acg gtg gaa cct ggg ctt att gaa tgc gat   403
Ala His Gly Leu Glu Leu Thr Val Glu Pro Gly Leu Ile Glu Cys Asp
                 90                  95                 100

ttc ggc gag tgg acg ggc cgg aaa cta act gag ctc aat gcc cta gag   451
Phe Gly Glu Trp Thr Gly Arg Lys Leu Thr Glu Leu Asn Ala Leu Glu
            105                 110                 115

gag tgg aaa gcg gtg cag aag aca ccg tct acc ttc agg ttt cca ggt   499
Glu Trp Lys Ala Val Gln Lys Thr Pro Ser Thr Phe Arg Phe Pro Gly
        120                 125                 130

ggt gag agt ttc gtg gaa atg cag gat cgg atg gtg gag gct atc ggc   547
Gly Glu Ser Phe Val Glu Met Gln Asp Arg Met Val Glu Ala Ile Gly
    135                 140                 145

aac att gcg cag cag cat ccg gga gaa atc gtt gct gcg ttt agt cat   595
Asn Ile Ala Gln Gln His Pro Gly Glu Ile Val Ala Ala Phe Ser His
150                 155                 160                 165

gcc gac acg atc aag gct gcg gtg gct cat ttt gta ggc act cca ctg   643
Ala Asp Thr Ile Lys Ala Ala Val Ala His Phe Val Gly Thr Pro Leu
                170                 175                 180

gat tct ttt cag cgc att ttc atc gac acg gcg tca att tcc gca gtg   691
Asp Ser Phe Gln Arg Ile Phe Ile Asp Thr Ala Ser Ile Ser Ala Val
            185                 190                 195

gaa ttt acc ggg aaa tct tca ggc gtc tcc tcc cat atg ctg ctg aca   739
Glu Phe Thr Gly Lys Ser Ser Gly Val Ser Ser His Met Leu Leu Thr
        200                 205                 210

aat tcc aga aca gga tcg ttg gga tac ctt cga gac aaa ctt ccg aaa   787
Asn Ser Arg Thr Gly Ser Leu Gly Tyr Leu Arg Asp Lys Leu Pro Lys
    215                 220                 225

gct ccg caa cca tgatcacctc accatttgag cgc                        822
Ala Pro Gln Pro
230
```

<210> 52
<211> 233
<212> PRT
<213> Corynebacterium glutamicum

<400> 52

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Met Leu His Val Met Lys Pro Gly Ser His Ala Ala Ala Glu Lys Thr
  1               5                  10                  15

Gln Ser Thr Val Val Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr
             20                  25                  30

Gly Gln Val Leu Pro Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys
         35                  40                  45

Gly Glu Glu Gln Ala Arg Glu Val Ala Gln Arg Leu Ala Glu Val Pro
     50                  55                  60

Ile Thr Ala Val Tyr Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala
 65                  70                  75                  80
```

```
Ala Pro Thr Val Ser Ala His Gly Leu Glu Leu Thr Val Glu Pro Gly
                 85                  90                  95

Leu Ile Glu Cys Asp Phe Gly Glu Trp Thr Gly Arg Lys Leu Thr Glu
            100                 105                 110

Leu Asn Ala Leu Glu Glu Trp Lys Ala Val Gln Lys Thr Pro Ser Thr
        115                 120                 125

Phe Arg Phe Pro Gly Gly Glu Ser Phe Val Glu Met Gln Asp Arg Met
    130                 135                 140

Val Glu Ala Ile Gly Asn Ile Ala Gln Gln His Pro Gly Glu Ile Val
145                 150                 155                 160

Ala Ala Phe Ser His Ala Asp Thr Ile Lys Ala Ala Val Ala His Phe
                165                 170                 175

Val Gly Thr Pro Leu Asp Ser Phe Gln Arg Ile Phe Ile Asp Thr Ala
            180                 185                 190

Ser Ile Ser Ala Val Glu Phe Thr Gly Lys Ser Ser Gly Val Ser Ser
        195                 200                 205

His Met Leu Leu Thr Asn Ser Arg Thr Gly Ser Leu Gly Tyr Leu Arg
    210                 215                 220

Asp Lys Leu Pro Lys Ala Pro Gln Pro
225                 230
```

<210> 53
<211> 1161
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1138)
<223> RXA00206

<400> 53

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ttaaataaga tggtcagaga cagtttttg gcctgtcaac ccctgtgatt ctcttatttt 60

tgggtgattg ttccggcgcg ggtgttgtga tgggtttaat atg gaa gac atg cga   115
                                        Met Glu Asp Met Arg
                                          1               5

att gct act ctc acg tca ggc ggc gac tgc ccc gga cta aac gcc gtc   163
Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val
                 10                  15                  20

atc cga gga atc gtc cgc aca gcc agc aat gaa ttt ggc tcc acc gtc   211
Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val
            25                  30                  35

gtt ggt tat caa gac ggt tgg gaa gga ctg tta ggc gat cgt cgc gta   259
Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu Gly Asp Arg Arg Val
        40                  45                  50
```

```
cag ctg tat gac gat gaa gat att gac cga atc ctc ctt cga ggc ggc   307
Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly
     55                  60                  65

acc att ttg ggc act ggt cgc ctc cat ccg gac aag ttt aag gcc gga   355
Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp Lys Phe Lys Ala Gly
 70                  75                  80                  85

att gat cag att aag gcc aac tta gaa gac gcc ggc atc gat gcc ctt   403
Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala Gly Ile Asp Ala Leu
                 90                  95                 100

atc cca atc ggt ggc gaa gga acc ctg aag ggt gcc aag tgg ctg tct   451
Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ser
            105                 110                 115

gat aac ggt atc cct gtt gtc ggt gtc cca aag acc att gac aat gac   499
Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp
        120                 125                 130

gtg aat ggc act gac ttc acc ttc ggt ttc gat act gct gtg gca gtg   547
Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp Thr Ala Val Ala Val
    135                 140                 145

gct acc gac gct gtt gac cgc ctg cac acc acc gct gaa tct cac aac   595
Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser His Asn
150                 155                 160                 165

cgt gtg atg atc gtg gag gtc atg ggc cgc cac gtg ggt tgg att gct   643
Arg Val Met Ile Val Glu Val Met Gly Arg His Val Gly Trp Ile Ala
                170                 175                 180

ctg cac gca ggt atg gcc ggc ggt gct cac tac acc gtt att cca gaa   691
Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu
            185                 190                 195

gta cct ttc gat att gca gag atc tgc aag gcg atg gaa cgt cgc ttc   739
Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala Met Glu Arg Arg Phe
        200                 205                 210

cag atg ggc gag aag tac ggc att atc gtc gtt gcg gaa ggt gcg ttg   787
Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu
    215                 220                 225

cca cgc gaa ggc acc atg gag ctt cgt gaa ggc cac att gac cag ttc   835
Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly His Ile Asp Gln Phe
230                 235                 240                 245

ggt cac aag acc ttc acg gga att gga cag cag atc gct gat gag atc   883
Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Ile
                250                 255                 260

cac gtg cgc ctc ggc cac gat gtt cgt acg acc gtt ctt ggc cac att   931
His Val Arg Leu Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile
            265                 270                 275

caa cgt ggt gga acc cca act gct ttc gac cgt gtt ctg gcc act cgt   979
Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg
        280                 285                 290

tat ggt gtt cgt gca gct cgt gcg tgc cat gag gga agc ttt gac aag   1027
```

```
Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu Gly Ser Phe Asp Lys
    295                 300                 305

gtt gtt gct ttg aag ggt gag agc att gag atg atc acc ttt gaa gaa   1075
Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met Ile Thr Phe Glu Glu
310                 315                 320                 325

gca gtc gga acc ttg aag gaa gtt cca ttc gaa cgc tgg gtt act gcc   1123
Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu Arg Trp Val Thr Ala
                330                 335                 340

cag gca atg ttt gga tagtttttcg ggcttttatc aac                    1161
Gln Ala Met Phe Gly
            345


<210> 54
<211> 346
<212> PRT
<213> Corynebacterium glutamicum

<400> 54
Met Glu Asp Met Arg Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro
  1               5                  10                  15

Gly Leu Asn Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu
             20                  25                  30

Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu
         35                  40                  45

Gly Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile
     50                  55                  60

Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp
 65                  70                  75                  80

Lys Phe Lys Ala Gly Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala
                 85                  90                  95

Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly
            100                 105                 110

Ala Lys Trp Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys
        115                 120                 125

Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp
    130                 135                 140

Thr Ala Val Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr
145                 150                 155                 160

Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His
                165                 170                 175

Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr
            180                 185                 190

Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala
        195                 200                 205
```

```
Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val
    210                 215                 220

Ala Glu Gly Ala Leu Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly
225                 230                 235                 240

His Ile Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln
                245                 250                 255

Ile Ala Asp Glu Ile His Val Arg Leu Gly His Asp Val Arg Thr Thr
            260                 265                 270

Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg
        275                 280                 285

Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu
    290                 295                 300

Gly Ser Phe Asp Lys Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met
305                 310                 315                 320

Ile Thr Phe Glu Glu Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu
                325                 330                 335

Arg Trp Val Thr Ala Gln Ala Met Phe Gly
            340                 345


<210> 55
<211> 1083
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1060)
<223> RXA01243

<400> 55
gcgcaatcag cgatatcgat gtggtggtca ccgatgcggg tgcaccagca agtttcgttg 60

agcagttgcg agaacgcgat gtagaagttg tgattgcaga atg att ctt aca gtc   115
                                        Met Ile Leu Thr Val
                                          1               5

act gca agt ccg tat ctg ttg agc acc aat gag ctt gac ggc acc atc   163
Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu Leu Asp Gly Thr Ile
                 10                  15                  20

gaa att ggc gaa gca aac aaa atc cgg cag gtt tcc act gtt gcc ggt   211
Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val Ser Thr Val Ala Gly
             25                  30                  35

ggt ttt ggc acc ggt gtg gct gcc acc ttg ttt tat ggc ggc aat gaa   259
Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe Tyr Gly Gly Asn Glu
         40                  45                  50

act ttt gca gtt ttt ccc gct cca gaa atc tct cat tac atg cgc ctg   307
Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser His Tyr Met Arg Leu
     55                  60                  65
```

```
gtg acg ttt gct ggg ttg cct cat gaa att att ccg gtg gca ggt ccc   355
Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile Pro Val Ala Gly Pro
 70                  75                  80                  85

atc ccc atg cat ttg acc atg cgt gat gca gag ggc aat gag act aag   403
Ile Pro Met His Leu Thr Met Arg Asp Ala Glu Gly Asn Glu Thr Lys
                90                  95                 100

ttc aaa gac tcc ccc atg cct ttg gat gtg tcc cag ttg gca att ctt   451
Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser Gln Leu Ala Ile Leu
            105                 110                 115

cgt gat cta gtg gtg cgt cga gcc gaa gat gcc gcg tgg gtg ttg ttg   499
Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala Ala Trp Val Leu Leu
        120                 125                 130

ggt ggc aat ttg ccg tct atc gcg cct gct gcg tgg ttt gtg gat gtg   547
Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala Trp Phe Val Asp Val
    135                 140                 145

gtg aga tca ctt cgc ttg tac cac cct cat gtg aag gta gct atc gca   595
Val Arg Ser Leu Arg Leu Tyr His Pro His Val Lys Val Ala Ile Ala
150                 155                 160                 165

gca act ggt gct gcg ttg cgt gcg gtt att cga cag ctt gca gct acg   643
Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg Gln Leu Ala Ala Thr
                170                 175                 180

tcc ccg gat gcg ctg att gtg gct gcg gaa gaa atc gaa att gcc act   691
Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu Ile Glu Ile Ala Thr
            185                 190                 195

gga tta gaa ccc aaa acc ttg aga ggt cca tgg gta gag gga gat ctc   739
Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp Val Glu Gly Asp Leu
        200                 205                 210

tcc ccg act gtg gcg gca gcg cgc gct tta att gat agc ggt gtc acc   787
Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile Asp Ser Gly Val Thr
    215                 220                 225

gag gtg ttg gtt acc aac aag cgg acg gaa tct ttg tat gtt tcc gag   835
Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser Leu Tyr Val Ser Glu
230                 235                 240                 245

tct gaa tca ctg tta gcc agc tac gac agc acc cct ggt aag cag ggc   883
Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr Pro Gly Lys Gln Gly
                250                 255                 260

gtg aat tgg cgg gaa tct ttt act gca gga ttc ttg gca gca tcc aat   931
Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe Leu Ala Ala Ser Asn
            265                 270                 275

gat gga aaa tcc act gag gac agc gtg atc aac gcg gtt gct tac gcc   979
Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn Ala Val Ala Tyr Ala
        280                 285                 290

aac gct gaa ggc agt gag tgg gac aac tac att ccc aca ccc gat aag   1027
Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile Pro Thr Pro Asp Lys
    295                 300                 305

ctt cgg gcg gag cac gtg gtc atc aaa tcg ctt tagaccacgc aaaaagcctc 1080
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Leu Arg Ala Glu His Val Val Ile Lys Ser Leu
310 315 320

aaa 1083

<210> 56
<211> 320
<212> PRT
<213> Corynebacterium glutamicum

<400> 56
Met Ile Leu Thr Val Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu
1 5 10 15

Leu Asp Gly Thr Ile Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val
20 25 30

Ser Thr Val Ala Gly Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe
35 40 45

Tyr Gly Gly Asn Glu Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser
50 55 60

His Tyr Met Arg Leu Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile
65 70 75 80

Pro Val Ala Gly Pro Ile Pro Met His Leu Thr Met Arg Asp Ala Glu
85 90 95

Gly Asn Glu Thr Lys Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser
100 105 110

Gln Leu Ala Ile Leu Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala
115 120 125

Ala Trp Val Leu Leu Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala
130 135 140

Trp Phe Val Asp Val Val Arg Ser Leu Arg Leu Tyr His Pro His Val
145 150 155 160

Lys Val Ala Ile Ala Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg
165 170 175

Gln Leu Ala Ala Thr Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu
180 185 190

Ile Glu Ile Ala Thr Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp
195 200 205

Val Glu Gly Asp Leu Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile
210 215 220

Asp Ser Gly Val Thr Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser
225 230 235 240

Leu Tyr Val Ser Glu Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr
245 250 255

Pro Gly Lys Gln Gly Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe

```
            260                 265                 270

Leu Ala Ala Ser Asn Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn
        275                 280                 285

Ala Val Ala Tyr Ala Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile
    290                 295                 300

Pro Thr Pro Asp Lys Leu Arg Ala Glu His Val Val Ile Lys Ser Leu
305                 310                 315                 320
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<210> 57
<211> 1113
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1090)
<223> RXA01882

<400> 57

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acccttttc caccttggct gattttgatg cccttgttac cgatgaccac acgctagatt 60

ttccagtttt gcccgaccac aactttcagg tggtaacccc atg atc atc aca ttc   115
                                            Met Ile Ile Thr Phe
                                              1               5

acc cca aac ccg agt att gat tcc acg ctg tcg ctc ggc gaa gag ctc   163
Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser Leu Gly Glu Glu Leu
                10                  15                  20

tcc cgt gga tcc gtc caa cga ctt gat tcc gtc acc gct gtc gca ggt   211
Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val Thr Ala Val Ala Gly
            25                  30                  35

ggt aaa ggc atc aat gtc gcc cac gct gtc ttg ctt gcg ggc ttt gaa   259
Gly Lys Gly Ile Asn Val Ala His Ala Val Leu Leu Ala Gly Phe Glu
        40                  45                  50

acc ttg gct gtg ttc cca gcc ggc aag ctc gac ccc ttc gtc cca ctg   307
Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp Pro Phe Val Pro Leu
    55                  60                  65

gtc cgc gac atc ggc ttg ccc gtg gaa act gtt gtg atc aac aag aac   355
Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val Val Ile Asn Lys Asn
70                  75                  80                  85

gtc cgc acc aac acc aca gtc acc gaa ccg gac ggc acc acc acc aag   403
Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp Gly Thr Thr Thr Lys
                90                  95                  100

ctc aac ggc ccc ggc gcg ccg ctc agc gag cag aag ctc cgt agc ttg   451
Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln Lys Leu Arg Ser Leu
            105                 110                 115

gaa aag gtg ctt atc gac gcg ctc cgc ccc gaa gtc acc tgg gtt gtc   499
```

```
Glu Lys Val Leu Ile Asp Ala Leu Arg Pro Glu Val Thr Trp Val Val
        120                 125                 130

ctg gcg ggc tcg ctg cca cca ggg gca cca gtt gac tgg tac gcg cgt   547
Leu Ala Gly Ser Leu Pro Pro Gly Ala Pro Val Asp Trp Tyr Ala Arg
    135                 140                 145

ctc acc gcg ttg atc cat tca gca cgc cct gac gtt cgc gtg gct gtc   595
Leu Thr Ala Leu Ile His Ser Ala Arg Pro Asp Val Arg Val Ala Val
150                 155                 160                 165

gat acc tca gac aag cca ctg atg gcg ttg ggc gag agc ttg gat aca   643
Asp Thr Ser Asp Lys Pro Leu Met Ala Leu Gly Glu Ser Leu Asp Thr
                170                 175                 180

cct ggc gct gct ccg aac ctg att aag cca aat ggt ctg gaa ctg ggc   691
Pro Gly Ala Ala Pro Asn Leu Ile Lys Pro Asn Gly Leu Glu Leu Gly
            185                 190                 195

cag ctg gct aac act gat ggt gaa gag ctg gag gcg cgt gct gcg caa   739
Gln Leu Ala Asn Thr Asp Gly Glu Glu Leu Glu Ala Arg Ala Ala Gln
        200                 205                 210

ggc gat tac gac gcc atc atc gca gct gcg gac gta ctg gtt aac cgt   787
Gly Asp Tyr Asp Ala Ile Ile Ala Ala Ala Asp Val Leu Val Asn Arg
    215                 220                 225

ggc atc gaa cag gtg ctt gtc acc ttg ggt gcc gca gga gcg gtg ttg   835
Gly Ile Glu Gln Val Leu Val Thr Leu Gly Ala Ala Gly Ala Val Leu
230                 235                 240                 245

gtc aac gca gaa ggt gcg tgg act gct act tct cca aag att gat gtt   883
Val Asn Ala Glu Gly Ala Trp Thr Ala Thr Ser Pro Lys Ile Asp Val
                250                 255                 260

gta tcc acc gtt gga gct gga gac tgt gct ctt gca ggt ttt gtt atg   931
Val Ser Thr Val Gly Ala Gly Asp Cys Ala Leu Ala Gly Phe Val Met
            265                 270                 275

gca cgt tcc cag aag aaa aca ctg gag gaa tct ctg ctg aat gcc gtg   979
Ala Arg Ser Gln Lys Lys Thr Leu Glu Glu Ser Leu Leu Asn Ala Val
        280                 285                 290

tct tac ggc tcg act gcg gcg tct ctt cct ggc act acc att cct cgt   1027
Ser Tyr Gly Ser Thr Ala Ala Ser Leu Pro Gly Thr Thr Ile Pro Arg
    295                 300                 305

cct gac caa ctc gcc aca gct ggt gca acg gtc acc caa gtc aaa gga   1075
Pro Asp Gln Leu Ala Thr Ala Gly Ala Thr Val Thr Gln Val Lys Gly
310                 315                 320                 325

ttg aaa gaa tca gca tgaatagcgt aaataattcc tcg                    1113
Leu Lys Glu Ser Ala
                330
```

<210> 58
<211> 330
<212> PRT
<213> Corynebacterium glutamicum

<400> 58

```
Met Ile Ile Thr Phe Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser
  1               5                  10                  15

Leu Gly Glu Glu Leu Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val
             20                  25                  30

Thr Ala Val Ala Gly Gly Lys Gly Ile Asn Val Ala His Ala Val Leu
         35                  40                  45

Leu Ala Gly Phe Glu Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp
     50                  55                  60

Pro Phe Val Pro Leu Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val
 65                  70                  75                  80

Val Ile Asn Lys Asn Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp
                 85                  90                  95

Gly Thr Thr Thr Lys Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln
            100                 105                 110

Lys Leu Arg Ser Leu Glu Lys Val Leu Ile Asp Ala Leu Arg Pro Glu
        115                 120                 125

Val Thr Trp Val Val Leu Ala Gly Ser Leu Pro Pro Gly Ala Pro Val
    130                 135                 140

Asp Trp Tyr Ala Arg Leu Thr Ala Leu Ile His Ser Ala Arg Pro Asp
145                 150                 155                 160

Val Arg Val Ala Val Asp Thr Ser Asp Lys Pro Leu Met Ala Leu Gly
                165                 170                 175

Glu Ser Leu Asp Thr Pro Gly Ala Ala Pro Asn Leu Ile Lys Pro Asn
            180                 185                 190

Gly Leu Glu Leu Gly Gln Leu Ala Asn Thr Asp Gly Glu Glu Leu Glu
        195                 200                 205

Ala Arg Ala Ala Gln Gly Asp Tyr Asp Ala Ile Ile Ala Ala Ala Asp
    210                 215                 220

Val Leu Val Asn Arg Gly Ile Glu Gln Val Leu Val Thr Leu Gly Ala
225                 230                 235                 240

Ala Gly Ala Val Leu Val Asn Ala Glu Gly Ala Trp Thr Ala Thr Ser
                245                 250                 255

Pro Lys Ile Asp Val Val Ser Thr Val Gly Ala Gly Asp Cys Ala Leu
            260                 265                 270

Ala Gly Phe Val Met Ala Arg Ser Gln Lys Lys Thr Leu Glu Glu Ser
        275                 280                 285

Leu Leu Asn Ala Val Ser Tyr Gly Ser Thr Ala Ala Ser Leu Pro Gly
    290                 295                 300

Thr Thr Ile Pro Arg Pro Asp Gln Leu Ala Thr Ala Gly Ala Thr Val
305                 310                 315                 320
```

```
Thr Gln Val Lys Gly Leu Lys Glu Ser Ala
                325                 330
```

<210> 59
<211> 1155
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1132)
<223> RXA01702

<400> 59

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attgtgaatg tgggattatc ggttcgcgct tcaccatgtt tctgcatgat gaaattacat 60

acatagttca gtgacagtca ccttttggag gagacacctt atg cct atc gca act   115
                                            Met Pro Ile Ala Thr
                                              1               5

ccc gag gtc tat aac gag atg ctc gat cgt gct aag gaa ggc gga ttc   163
Pro Glu Val Tyr Asn Glu Met Leu Asp Arg Ala Lys Glu Gly Gly Phe
                10                  15                  20

gcc ttc cca gcc atc aac tgc acc tcc tcg gaa acc atc aac gca gct   211
Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu Thr Ile Asn Ala Ala
            25                  30                  35

ctc aag ggc ttc gca gag gct gaa tct gac gga atc atc cag ttc tcc   259
Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly Ile Ile Gln Phe Ser
        40                  45                  50

acc ggt ggt gca gag ttc ggt tcc ggc ctg gca gta aag aac aag gtc   307
Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala Val Lys Asn Lys Val
    55                  60                  65

aag ggc gca gtt gcg ctt gca gcc ttc gcc cac gag gca gca aag agc   355
Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His Glu Ala Ala Lys Ser
70                  75                  80                  85

tac ggc atc aac gtt gct ctg cac act gac cac tgc cag aag gaa gtc   403
Tyr Gly Ile Asn Val Ala Leu His Thr Asp His Cys Gln Lys Glu Val
                90                  95                  100

ctg gac gag tac gtc cgc cca ctg ctg gct atc tcc cag gag cgc gtc   451
Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile Ser Gln Glu Arg Val
            105                 110                 115

gac cgc ggc gag ctt cca ctg ttc cag tcc cac atg tgg gat ggt tcc   499
Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His Met Trp Asp Gly Ser
        120                 125                 130

gct gtc cca atc gac gag aac ctc gaa atc gca cag gag ctg ctg gct   547
Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala Gln Glu Leu Leu Ala
    135                 140                 145

aag gcc aag gca gcg aac atc atc ttg gaa gtt gag atc ggt gtt gtc   595
Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val Glu Ile Gly Val Val
150                 155                 160                 165
```

```
ggt ggc gaa gaa gac ggc gtt gag gct aag gct ggc gca aac ctc tac   643
Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala Gly Ala Asn Leu Tyr
                170                 175                 180

acc tcc cca gaa gac ttt gag aag acc atc gat gca atc ggc acc ggt   691
Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp Ala Ile Gly Thr Gly
            185                 190                 195

gag aag ggc cgc tac ctg cta gca gct acc ttc ggt aac gtc cac ggc   739
Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe Gly Asn Val His Gly
        200                 205                 210

gtt tac aag cca ggc aac gtc aag ctg cgc cca gag gtc ctc ctt gag   787
Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro Glu Val Leu Leu Glu
    215                 220                 225

ggc cag cag gtt gca cgc aag aag ctt gga ctt gca gac gac gca ctt   835
Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu Ala Asp Asp Ala Leu
230                 235                 240                 245

cca ttc gac ttc gtc ttc cac ggt ggc tca ggc tcc gag aag gaa aag   883
Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly Ser Glu Lys Glu Lys
                250                 255                 260

atc gaa gag gcg ctg acc tac ggc gtc atc aag atg aac gtt gat act   931
Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys Met Asn Val Asp Thr
            265                 270                 275

gac acc cag tac gca ttc acc cgc cca atc gtc tcc cac atg ttt gag   979
Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val Ser His Met Phe Glu
        280                 285                 290

aac tac aac ggc gtt ctc aag atc gac ggc gag gtc gga aac aag aag   1027
Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu Val Gly Asn Lys Lys
    295                 300                 305

gct tac gac cca cgc tct tac atg aag aag gct gag cag agc atg tct   1075
Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala Glu Gln Ser Met Ser
310                 315                 320                 325

gag cgc att atc gag tct tgc cag gac ctc aag tct gtt gga aag acc   1123
Glu Arg Ile Ile Glu Ser Cys Gln Asp Leu Lys Ser Val Gly Lys Thr
                330                 335                 340

acc tct aag taatctcagc agttaaaaag ggc                            1155
Thr Ser Lys
```

<210> 60
<211> 344
<212> PRT
<213> Corynebacterium glutamicum

<400> 60

```
Met Pro Ile Ala Thr Pro Glu Val Tyr Asn Glu Met Leu Asp Arg Ala
  1               5                  10                  15

Lys Glu Gly Gly Phe Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu
            20                  25                  30
```

```
Thr Ile Asn Ala Ala Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly
        35                  40                  45

Ile Ile Gln Phe Ser Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala
    50                  55                  60

Val Lys Asn Lys Val Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His
65                  70                  75                  80

Glu Ala Ala Lys Ser Tyr Gly Ile Asn Val Ala Leu His Thr Asp His
                85                  90                  95

Cys Gln Lys Glu Val Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile
            100                 105                 110

Ser Gln Glu Arg Val Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His
        115                 120                 125

Met Trp Asp Gly Ser Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala
    130                 135                 140

Gln Glu Leu Leu Ala Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val
145                 150                 155                 160

Glu Ile Gly Val Val Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala
                165                 170                 175

Gly Ala Asn Leu Tyr Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp
            180                 185                 190

Ala Ile Gly Thr Gly Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe
        195                 200                 205

Gly Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro
    210                 215                 220

Glu Val Leu Leu Glu Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu
225                 230                 235                 240

Ala Asp Asp Ala Leu Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly
                245                 250                 255

Ser Glu Lys Glu Lys Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys
            260                 265                 270

Met Asn Val Asp Thr Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val
        275                 280                 285

Ser His Met Phe Glu Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu
    290                 295                 300

Val Gly Asn Lys Lys Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala
305                 310                 315                 320

Glu Gln Ser Met Ser Glu Arg Ile Ile Glu Ser Cys Gln Asp Leu Lys
                325                 330                 335

Ser Val Gly Lys Thr Thr Ser Lys
            340
```

<210> 61
<211> 900
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(877)
<223> RXA02258

<400> 61
cgttgcaatt ctcgctcagt aaatccgaca cggccctttg ttagaaaaca aaacataaag 60

ggccaccggg aaacttttt aagaaaggtg tgtttcacac atg gca cgt aag cca 115
Met Ala Arg Lys Pro
1 5

ctt atc gct ggt aac tgg aag atg aac ctg gat cac cag cag gca atc 163
Leu Ile Ala Gly Asn Trp Lys Met Asn Leu Asp His Gln Gln Ala Ile
10 15 20

ggc act gtt cag aag ctt gca ttc gcc ctt cca aag gaa tac ttc gag 211
Gly Thr Val Gln Lys Leu Ala Phe Ala Leu Pro Lys Glu Tyr Phe Glu
25 30 35

aag gtt gac gtt gca gtc acc gtt cct ttc act gac atc cgc tcc gtc 259
Lys Val Asp Val Ala Val Thr Val Pro Phe Thr Asp Ile Arg Ser Val
40 45 50

cag act ctc gtt gag ggc gac aag ctt gag gtc act ttc ggt gct cag 307
Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val Thr Phe Gly Ala Gln
55 60 65

gac gtc tcc cag cac gag tcc ggt gcg tac acc ggt gaa gtt tct gca 355
Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr Gly Glu Val Ser Ala
70 75 80 85

agc atg ctg gca aag ttg aac tgc tct tgg gtt gtc gtt gga cac tcc 403
Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val Val Val Gly His Ser
90 95 100

gag cgc cgc gag tac cac aac gag tct gat gag ttg gtt gct gcg aag 451
Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu Leu Val Ala Ala Lys
105 110 115

gca aag gca gct ctg tcc aac ggc atc agc ccg atc gtc tgc gtt ggt 499
Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro Ile Val Cys Val Gly
120 125 130

gag cca ctg gaa atc cgt gaa gct ggc acc cac gtt gag tac gtc gtc 547
Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His Val Glu Tyr Val Val
135 140 145

gag cag acc cgt aag tcc ctt gct ggc ctg gat gct gct gag ctg gcc 595
Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp Ala Ala Glu Leu Ala
150 155 160 165

aac acc gtt atc gcg tat gag cca gtg tgg gct atc ggc acc ggt aag 643
Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala Ile Gly Thr Gly Lys
170 175 180

```
gtt gct tcc gca gct gac gct cag gaa gtg tgc aag gct atc cgc ggt   691
Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys Lys Ala Ile Arg Gly
            185                 190                 195

ctg atc gtg gag ctt gca ggc gac gag gtc gct gag ggc ctg cgt att   739
Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala Glu Gly Leu Arg Ile
        200                 205                 210

ctt tac ggt ggt tct gtt aag gca gaa acc gtc gct gag atc gtc ggt   787
Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val Ala Glu Ile Val Gly
    215                 220                 225

cag cct gac gtc gac ggc gga ctt gtc ggt ggc gct tcc ctc gac ggt   835
Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly Ala Ser Leu Asp Gly
230                 235                 240                 245

gaa gca ttc gcc aag ctg gct gcc aac gct gcg agc gtt gct           877
Glu Ala Phe Ala Lys Leu Ala Ala Asn Ala Ala Ser Val Ala
                250                 255

taaagtacag agctttaaag cac                                        900
```

<210> 62
<211> 259
<212> PRT
<213> Corynebacterium glutamicum

<400> 62

```
Met Ala Arg Lys Pro Leu Ile Ala Gly Asn Trp Lys Met Asn Leu Asp
  1               5                  10                  15

His Gln Gln Ala Ile Gly Thr Val Gln Lys Leu Ala Phe Ala Leu Pro
            20                  25                  30

Lys Glu Tyr Phe Glu Lys Val Asp Val Ala Val Thr Val Pro Phe Thr
        35                  40                  45

Asp Ile Arg Ser Val Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val
    50                  55                  60

Thr Phe Gly Ala Gln Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr
65                  70                  75                  80

Gly Glu Val Ser Ala Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val
                85                  90                  95

Val Val Gly His Ser Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu
            100                 105                 110

Leu Val Ala Ala Lys Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro
        115                 120                 125

Ile Val Cys Val Gly Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His
    130                 135                 140

Val Glu Tyr Val Val Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp
145                 150                 155                 160

Ala Ala Glu Leu Ala Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala
                165                 170                 175
```

```
Ile Gly Thr Gly Lys Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys
            180                 185                 190

Lys Ala Ile Arg Gly Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala
        195                 200                 205

Glu Gly Leu Arg Ile Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val
    210                 215                 220

Ala Glu Ile Val Gly Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly
225                 230                 235                 240

Ala Ser Leu Asp Gly Glu Ala Phe Ala Lys Leu Ala Ala Asn Ala Ala
                245                 250                 255

Ser Val Ala
```

<210> 63
<211> 1563
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1540)
<223> RXN01225

<400> 63

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tttgggctaa tgttgggggg agtgctttca actatccacg agagctgccc agtgataaac 60

cccgggttaa ccccacgcct aagtcagtga aggacttttt atg acg cac aac cac   115
                                            Met Thr His Asn His
                                              1               5

aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg   163
Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
                10                  15                  20

atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt   211
Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
            25                  30                  35

cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc   259
Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
        40                  45                  50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg   307
Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
    55                  60                  65

gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tcg atc   355
Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
70                  75                  80                  85

gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac   403
Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
                90                  95                  100
```

```
ctg cgt gcc ttc ctg gag gac gct ctc gcg ccg gtc att ggt gcg gaa   451
Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro Val Ile Gly Ala Glu
            105                 110                 115

acc gac atc aac cca act gat atc gtg ctg tac ggt ttc ggc cgc atc   499
Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr Gly Phe Gly Arg Ile
        120                 125                 130

ggt cgc ctg ctg gcc cgc atc ctg gtt tcc cgc gag gca ctg tat gac   547
Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg Glu Ala Leu Tyr Asp
    135                 140                 145

ggt gct cgt ctg cgc gcc atc gtg gtc cgc aaa aat ggt gaa gaa gac   595
Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp
150                 155                 160                 165

ctg gtc aag cgc gca tcc ttg ctg cgt cgt gat tct gtc cac ggt gga   643
Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly
                170                 175                 180

ttc gat ggc acc atc acc acc gat tat gac aac aac atc atc tgg gcc   691
Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala
            185                 190                 195

aac ggc acc cca atc aag gtc atc tac tcc aat gac cca gcc acc att   739
Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile
        200                 205                 210

gat tac acc gaa tac ggc atc aat gac gcc gtc gtg gta gac aac acc   787
Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr
    215                 220                 225

ggc cgc tgg cgt gac cgc gaa ggc ctg tcc cag cac ctc aag tcc aag   835
Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln His Leu Lys Ser Lys
230                 235                 240                 245

ggc gtt gcc aag gtt gta ctc acc gcg ccg ggc aag ggc gat ctg aag   883
Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys
                250                 255                 260

aac atc gtg tac ggc atc aac cac acc gac atc acc gca gat gat cag   931
Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln
            265                 270                 275

atc gtt tcc gca gca tca tgc acc acc aat gcc att acc cca gtg ctc   979
Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu
        280                 285                 290

aag gtg atc aat gat cgc tac ggc gtg gaa ttc ggc cac gta gaa acc   1027
Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr
    295                 300                 305

gtt cac tcc ttc acc aat gac cag aac ctg atc gac aac ttc cac aag   1075
Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile Asp Asn Phe His Lys
310                 315                 320                 325

ggt tct cgc cgt ggt cgc gca gca ggt ctg aat atg gtt ctc acc gaa   1123
Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn Met Val Leu Thr Glu
                330                 335                 340

acc ggc gct gca aag gct gta tcc aag gcg ctt cca gag ctg gaa ggc   1171
```

```
Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly
            345                 350                 355

aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg   1219
Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met
        360                 365                 370

gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc   1267
Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val
    375                 380                 385

aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa   1315
Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln
390                 395                 400                 405

atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc   1363
Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly
                410                 415                 420

acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt   1411
Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly
            425                 430                 435

cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc   1459
Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser
        440                 445                 450

aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc   1507
Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg
    455                 460                 465

gtg tac ccg gag cgc agg cag cca gcc gta cta taggttatcc aagcctaata 1560
Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
470                 475                 480

cac                                                               1563


<210> 64
<211> 480
<212> PRT
<213> Corynebacterium glutamicum

<400> 64
Met Thr His Asn His Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu
  1               5                  10                  15

Glu Met Val Pro Leu Ile Gly Arg Leu His Arg Asn Asn Asn Val Val
             20                  25                  30

Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile
         35                  40                  45

Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro
     50                  55                  60

Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu
 65                  70                  75                  80

Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
                 85                  90                  95
```

```
Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro
            100                 105                 110

Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr
        115                 120                 125

Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg
    130                 135                 140

Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys
145                 150                 155                 160

Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp
                165                 170                 175

Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn
            180                 185                 190

Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn
        195                 200                 205

Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val
    210                 215                 220

Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
225                 230                 235                 240

His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
                245                 250                 255

Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile
            260                 265                 270

Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala
        275                 280                 285

Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe
    290                 295                 300

Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile
305                 310                 315                 320

Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
                325                 330                 335

Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu
            340                 345                 350

Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr
        355                 360                 365

Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val
    370                 375                 380

Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser
385                 390                 395                 400

Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
                405                 410                 415
```

```
Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
            420                 425                 430

Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn
        435                 440                 445

Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala
    450                 455                 460

Gly Val Arg Pro Arg Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
465                 470                 475                 480
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<210> 65
<211> 1563
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1540)
<223> FRXA01225

<400> 65

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tttgggctaa tgttgggggg agtgctttca actatccacg agagctgccc agtgataaac 60

cccgggttaa ccccacgcct aagtcagtga aggacttttt atg acg cac aac cac   115
                                            Met Thr His Asn His
                                              1               5

aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg   163
Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
                10                  15                  20

atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt   211
Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
            25                  30                  35

cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc   259
Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
        40                  45                  50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg   307
Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
    55                  60                  65

gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tcg atc   355
Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
70                  75                  80                  85

gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac   403
Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
                90                  95                  100

ctg cgt gcc ttc ctg gag gac gct ctc gcg ccg gtc att ggt gcg gaa   451
Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro Val Ile Gly Ala Glu
            105                 110                 115
```

```
acc gac atc aac cca act gat atc gtg ctg tac ggt ttc ggc cgc atc   499
Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr Gly Phe Gly Arg Ile
        120                 125                 130

ggt cgc ctg ctg gcc cgc atc ctg gtt tcc cgc gag gca ctg tat gac   547
Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg Glu Ala Leu Tyr Asp
    135                 140                 145

ggt gct cgt ctg cgc gcc atc gtg gtc cgc aaa aat ggt gaa gaa gac   595
Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp
150                 155                 160                 165

ctg gtc aag cgc gca tcc ttg ctg cgt cgt gat tct gtc cac ggt gga   643
Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly
                170                 175                 180

ttc gat ggc acc atc acc acc gat tat gac aac aac atc atc tgg gcc   691
Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala
            185                 190                 195

aac ggc acc cca atc aag gtc atc tac tcc aat gac cca gcc acc att   739
Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile
        200                 205                 210

gat tac acc gaa tac ggc atc aat gac gcc gtc gtg gta gac aac acc   787
Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr
    215                 220                 225

ggc cgc tgg cgt gac cgc gaa ggc ctg tcc cag cac ctc aag tcc aag   835
Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln His Leu Lys Ser Lys
230                 235                 240                 245

ggc gtt gcc aag gtt gta ctc acc gcg ccg ggc aag ggc gat ctg aag   883
Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys
                250                 255                 260

aac atc gtg tac ggc atc aac cac acc gac atc acc gca gat gat cag   931
Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln
            265                 270                 275

atc gtt tcc gca gca tca tgc acc acc aat gcc att acc cca gtg ctc   979
Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu
        280                 285                 290

aag gtg atc aat gat cgc tac ggc gtg gaa ttc ggc cac gta gaa acc   1027
Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr
    295                 300                 305

gtt cac tcc ttc acc aat gac cag aac ctg atc gac aac ttc cac aag   1075
Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile Asp Asn Phe His Lys
310                 315                 320                 325

ggt tct cgc cgt ggt cgc gca gca ggt ctg aat atg gtt ctc acc gaa   1123
Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn Met Val Leu Thr Glu
                330                 335                 340

acc ggc gct gca aag gct gta tcc aag gcg ctt cca gag ctg gaa ggc   1171
Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly
            345                 350                 355

aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg   1219
```

```
Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met
        360                 365                 370

gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc   1267
Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val
    375                 380                 385

aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa   1315
Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln
390                 395                 400                 405

atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc   1363
Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly
                410                 415                 420

acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt   1411
Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly
            425                 430                 435

cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc   1459
Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser
        440                 445                 450

aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc   1507
Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg
    455                 460                 465

gtg tac ccg gag cgc agg cag cca gcc gta cta taggttatcc aagcctaata 1560
Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
470                 475                 480

cac                                                               1563
```

<210> 66
<211> 480
<212> PRT
<213> Corynebacterium glutamicum

<400> 66

```
Met Thr His Asn His Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu
  1               5                  10                  15

Glu Met Val Pro Leu Ile Gly Arg Leu His Arg Asn Asn Asn Val Val
             20                  25                  30

Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile
         35                  40                  45

Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro
     50                  55                  60

Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu
 65                  70                  75                  80

Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
                 85                  90                  95

Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro
            100                 105                 110
```

```
Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr
        115                 120                 125

Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg
    130                 135                 140

Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys
145                 150                 155                 160

Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp
                165                 170                 175

Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn
            180                 185                 190

Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn
        195                 200                 205

Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val
    210                 215                 220

Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
225                 230                 235                 240

His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
                245                 250                 255

Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile
            260                 265                 270

Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala
        275                 280                 285

Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe
    290                 295                 300

Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile
305                 310                 315                 320

Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
                325                 330                 335

Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu
            340                 345                 350

Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr
        355                 360                 365

Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val
    370                 375                 380

Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser
385                 390                 395                 400

Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
                405                 410                 415

Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
            420                 425                 430

Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn
```

```
        435                 440                 445

Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala
    450                 455                 460

Gly Val Arg Pro Arg Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
465                 470                 475                 480
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<210> 67
<211> 1125
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1102)
<223> RXA02256

<400> 67

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ttgggttctg tcagctcaag aattcttgag tgaccgatgc tctgattgac ctaactgctt 60

gacacattgc atttcctaca atctttagag gagacacaac atg acc att cgt gtt   115
                                            Met Thr Ile Arg Val
                                              1               5

ggt att aac gga ttt ggc cgt atc gga cgt aac ttc ttc cgc gca gtt   163
Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn Phe Phe Arg Ala Val
                 10                  15                  20

ctg gag cgc agc gac gat ctc gag gta gtt gca gtc aac gac ctc acc   211
Leu Glu Arg Ser Asp Asp Leu Glu Val Val Ala Val Asn Asp Leu Thr
             25                  30                  35

gac aac aag acc ctt tcc acc ctt ctc aag ttc gac tcc atc atg ggc   259
Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Phe Asp Ser Ile Met Gly
         40                  45                  50

cgc ctt ggc cag gaa gtt gaa tac gac gat gac tcc atc acc gtt ggt   307
Arg Leu Gly Gln Glu Val Glu Tyr Asp Asp Asp Ser Ile Thr Val Gly
     55                  60                  65

ggc aag cgc atc gct gtt tac gca gag cgc gat cca aag aac ctg gac   355
Gly Lys Arg Ile Ala Val Tyr Ala Glu Arg Asp Pro Lys Asn Leu Asp
 70                  75                  80                  85

tgg gct gca cac aac gtt gac atc gtg atc gag tcc acc ggc ttc ttc   403
Trp Ala Ala His Asn Val Asp Ile Val Ile Glu Ser Thr Gly Phe Phe
                 90                  95                 100

acc gat gca aac gcg gct aag gct cac atc gaa gca ggt gcc aag aag   451
Thr Asp Ala Asn Ala Ala Lys Ala His Ile Glu Ala Gly Ala Lys Lys
            105                 110                 115

gtc atc atc tcc gca cca gca agc aac gaa gac gca acc ttc gtt tac   499
Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp Ala Thr Phe Val Tyr
        120                 125                 130
```

```
ggt gtg aac cac gag tcc tac gat cct gag aac cac aac gtg atc tcc   547
Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn His Asn Val Ile Ser
    135                 140                 145

ggc gca tct tgc acc acc aac tgc ctc gca cca atg gca aag gtc cta   595
Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys Val Leu
150                 155                 160                 165

aac gac aag ttc ggc atc gag aac ggc ctc atg acc acc gtt cac gca   643
Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met Thr Thr Val His Ala
                170                 175                 180

tac act ggc gac cag cgc ctg cac gat gca cct cac cgc gac ctg cgt   691
Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro His Arg Asp Leu Arg
            185                 190                 195

cgt gca cgt gca gca gca gtc aac atc gtt cct acc tcc acc ggt gca   739
Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro Thr Ser Thr Gly Ala
        200                 205                 210

gct aag gct gtt gct ctg gtt ctc cca gag ctc aag ggc aag ctt gac   787
Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu Lys Gly Lys Leu Asp
    215                 220                 225

ggc tac gca ctt cgc gtt cca gtt atc acc ggt tcc gca acc gac ctg   835
Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly Ser Ala Thr Asp Leu
230                 235                 240                 245

acc ttc aac acc aag tct gag gtc acc gtt gag tcc atc aac gct gca   883
Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu Ser Ile Asn Ala Ala
                250                 255                 260

atc aag gaa gct gca gtc ggc gag ttc ggc gag acc ctg gct tac tcc   931
Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu Thr Leu Ala Tyr Ser
            265                 270                 275

gaa gag cca ctg gtt tcc acc gac atc gtc cac gat tcc cac ggc tcc   979
Glu Glu Pro Leu Val Ser Thr Asp Ile Val His Asp Ser His Gly Ser
        280                 285                 290

atc ttc gac gct ggc ctg acc aag gtc tcc ggc aac acc gtc aag gtt   1027
Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly Asn Thr Val Lys Val
    295                 300                 305

gtt tcc tgg tac gac aac gag tgg ggc tac acc tgc cag ctc ctg cgt   1075
Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr Cys Gln Leu Leu Arg
310                 315                 320                 325

ctg acc gag ctc gta gct tcc aag ctc taattagttc acatcgctaa        1122
Leu Thr Glu Leu Val Ala Ser Lys Leu
                330

cgt                                                              1125
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<210> 68
<211> 334
<212> PRT
<213> Corynebacterium glutamicum

<400> 68

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Met Thr Ile Arg Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn
 1               5                  10                  15

Phe Phe Arg Ala Val Leu Glu Arg Ser Asp Asp Leu Glu Val Val Ala
            20                  25                  30

Val Asn Asp Leu Thr Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Phe
        35                  40                  45

Asp Ser Ile Met Gly Arg Leu Gly Gln Glu Val Glu Tyr Asp Asp Asp
    50                  55                  60

Ser Ile Thr Val Gly Gly Lys Arg Ile Ala Val Tyr Ala Glu Arg Asp
65                  70                  75                  80

Pro Lys Asn Leu Asp Trp Ala Ala His Asn Val Asp Ile Val Ile Glu
                85                  90                  95

Ser Thr Gly Phe Phe Thr Asp Ala Asn Ala Ala Lys Ala His Ile Glu
            100                 105                 110

Ala Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp
        115                 120                 125

Ala Thr Phe Val Tyr Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn
    130                 135                 140

His Asn Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro
145                 150                 155                 160

Met Ala Lys Val Leu Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met
                165                 170                 175

Thr Thr Val His Ala Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro
            180                 185                 190

His Arg Asp Leu Arg Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro
        195                 200                 205

Thr Ser Thr Gly Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu
    210                 215                 220

Lys Gly Lys Leu Asp Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly
225                 230                 235                 240

Ser Ala Thr Asp Leu Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu
                245                 250                 255

Ser Ile Asn Ala Ala Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu
            260                 265                 270

Thr Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Thr Asp Ile Val His
        275                 280                 285

Asp Ser His Gly Ser Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly
    290                 295                 300

Asn Thr Val Lys Val Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr
305                 310                 315                 320

Cys Gln Leu Leu Arg Leu Thr Glu Leu Val Ala Ser Lys Leu
```

325 330

<210> 69
<211> 1338
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1315)
<223> RXA02257

<400> 69
ataccggtgc cagcgccaca caatgtgtgg caatctggga cagtgcatca cattgcacca 60

gaagaatttt ttaaacaatc aaatctccaa ggagtacggc atg gct gtt aag acc 115
Met Ala Val Lys Thr
1 5

ctc aag gac ttg ctc gac gaa ggc gta gac gga cgc cac gtc atc gtt 163
Leu Lys Asp Leu Leu Asp Glu Gly Val Asp Gly Arg His Val Ile Val
10 15 20

cga tct gac ttc aat gtt ccc ctc aac gat gac cgc gag atc acc gat 211
Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Asp Arg Glu Ile Thr Asp
25 30 35

aag ggc cga atc att gcc tcc cta cca acc ctt aaa gca ctg agc gaa 259
Lys Gly Arg Ile Ile Ala Ser Leu Pro Thr Leu Lys Ala Leu Ser Glu
40 45 50

ggt ggc gca aag gtc atc gtc atg gct cac ctt ggc cgc cca aag ggc 307
Gly Gly Ala Lys Val Ile Val Met Ala His Leu Gly Arg Pro Lys Gly
55 60 65

gag gtc aac gag aag tac tcc ctc gca cct gtc gct gag gca ctc tcc 355
Glu Val Asn Glu Lys Tyr Ser Leu Ala Pro Val Ala Glu Ala Leu Ser
70 75 80 85

gat gag ctt ggc cag tac gtt gca ctt gcc gca gac gtt gtt ggc gaa 403
Asp Glu Leu Gly Gln Tyr Val Ala Leu Ala Ala Asp Val Val Gly Glu
90 95 100

gac gca cac gag cgc gca aac ggc ctg acc gag ggc gac atc ctg ctc 451
Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu Gly Asp Ile Leu Leu
105 110 115

ctg gag aac gtg cgc ttc gac cca cgc gaa acc tcc aag gac gag gca 499
Leu Glu Asn Val Arg Phe Asp Pro Arg Glu Thr Ser Lys Asp Glu Ala
120 125 130

gag cgc acc gct ttc gct cag gag ctc gca gct ctt gca gca gac aac 547
Glu Arg Thr Ala Phe Ala Gln Glu Leu Ala Ala Leu Ala Ala Asp Asn
135 140 145

ggc gca ttc gtt tct gac ggc ttc ggt gtt gtc cac cgc gca cag acc 595
Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val His Arg Ala Gln Thr
150 155 160 165

tcc gtc tac gac att gca aag ttg ctg cca cac tac gct ggc gga ctg 643

```
Ser Val Tyr Asp Ile Ala Lys Leu Leu Pro His Tyr Ala Gly Gly Leu
                170                 175                 180

gta gag acc gag att tcc gtt ctg gaa aag atc gca gaa tca cca gag   691
Val Glu Thr Glu Ile Ser Val Leu Glu Lys Ile Ala Glu Ser Pro Glu
            185                 190                 195

gca cca tac gta gtg gtt ctc ggt gga tcc aag gtc tct gac aag atc   739
Ala Pro Tyr Val Val Val Leu Gly Gly Ser Lys Val Ser Asp Lys Ile
        200                 205                 210

ggt gtt att gag gcg ctg gct gcc aag gct gac aag atc atc gtc ggt   787
Gly Val Ile Glu Ala Leu Ala Ala Lys Ala Asp Lys Ile Ile Val Gly
    215                 220                 225

ggc ggc atg tgc tac acc ttc ctc gca gct cag gga cac aac gtt cag   835
Gly Gly Met Cys Tyr Thr Phe Leu Ala Ala Gln Gly His Asn Val Gln
230                 235                 240                 245

cag tcc ctc ctg cag gaa gaa atg aag gct acc tgc acc gac ctg ctc   883
Gln Ser Leu Leu Gln Glu Glu Met Lys Ala Thr Cys Thr Asp Leu Leu
                250                 255                 260

gca cgc ttc ggt gac aag atc gtt ctc cca gtt gac ctg gtt gca gca   931
Ala Arg Phe Gly Asp Lys Ile Val Leu Pro Val Asp Leu Val Ala Ala
            265                 270                 275

tcc gaa ttt aac aag gac gca gag aag cag atc gtt gac ctg gac tcc   979
Ser Glu Phe Asn Lys Asp Ala Glu Lys Gln Ile Val Asp Leu Asp Ser
        280                 285                 290

atc cca gaa ggc tgg atg tct ctt gac atc gga cca gag tcc gtc aag   1027
Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly Pro Glu Ser Val Lys
    295                 300                 305

aac ttc ggt gag gtt ctc agc acc gct aag acc atc ttc tgg aac ggc   1075
Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr Ile Phe Trp Asn Gly
310                 315                 320                 325

cca atg ggc gtg ttc gag ttc gca gca ttc tct gaa ggc acc cgc ggc   1123
Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser Glu Gly Thr Arg Gly
                330                 335                 340

atc gcc cag gcc atc atc gat gca act gca ggc aac gac gca ttc tcc   1171
Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly Asn Asp Ala Phe Ser
            345                 350                 355

gtt gtt ggc ggt ggc gac tcc gca gca tcc gtt cgc gtg ctc ggc ctg   1219
Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val Arg Val Leu Gly Leu
        360                 365                 370

aac gaa gac ggc ttc tcc cac atc tcc acc ggt ggt ggc gca tcc ctc   1267
Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly Gly Gly Ala Ser Leu
    375                 380                 385

gag tac ctt gaa ggc aag gaa ctc cca ggc gtt gca att ctc gct cag   1315
Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val Ala Ile Leu Ala Gln
390                 395                 400                 405

taaatccgac acggcccttt gtt                                        1338
```

<210> 70
<211> 405
<212> PRT
<213> Corynebacterium glutamicum

<400> 70

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Met Ala Val Lys Thr Leu Lys Asp Leu Leu Asp Glu Gly Val Asp Gly
  1               5                  10                  15

Arg His Val Ile Val Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Asp
             20                  25                  30

Arg Glu Ile Thr Asp Lys Gly Arg Ile Ile Ala Ser Leu Pro Thr Leu
         35                  40                  45

Lys Ala Leu Ser Glu Gly Gly Ala Lys Val Ile Val Met Ala His Leu
     50                  55                  60

Gly Arg Pro Lys Gly Glu Val Asn Glu Lys Tyr Ser Leu Ala Pro Val
 65                  70                  75                  80

Ala Glu Ala Leu Ser Asp Glu Leu Gly Gln Tyr Val Ala Leu Ala Ala
                 85                  90                  95

Asp Val Val Gly Glu Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu
            100                 105                 110

Gly Asp Ile Leu Leu Leu Glu Asn Val Arg Phe Asp Pro Arg Glu Thr
        115                 120                 125

Ser Lys Asp Glu Ala Glu Arg Thr Ala Phe Ala Gln Glu Leu Ala Ala
    130                 135                 140

Leu Ala Ala Asp Asn Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val
145                 150                 155                 160

His Arg Ala Gln Thr Ser Val Tyr Asp Ile Ala Lys Leu Leu Pro His
                165                 170                 175

Tyr Ala Gly Gly Leu Val Glu Thr Glu Ile Ser Val Leu Glu Lys Ile
            180                 185                 190

Ala Glu Ser Pro Glu Ala Pro Tyr Val Val Val Leu Gly Gly Ser Lys
        195                 200                 205

Val Ser Asp Lys Ile Gly Val Ile Glu Ala Leu Ala Ala Lys Ala Asp
    210                 215                 220

Lys Ile Ile Val Gly Gly Gly Met Cys Tyr Thr Phe Leu Ala Ala Gln
225                 230                 235                 240

Gly His Asn Val Gln Gln Ser Leu Leu Gln Glu Glu Met Lys Ala Thr
                245                 250                 255

Cys Thr Asp Leu Leu Ala Arg Phe Gly Asp Lys Ile Val Leu Pro Val
            260                 265                 270

Asp Leu Val Ala Ala Ser Glu Phe Asn Lys Asp Ala Glu Lys Gln Ile
        275                 280                 285
```

```
Val Asp Leu Asp Ser Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly
    290                 295                 300

Pro Glu Ser Val Lys Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr
305                 310                 315                 320

Ile Phe Trp Asn Gly Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser
                325                 330                 335

Glu Gly Thr Arg Gly Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly
            340                 345                 350

Asn Asp Ala Phe Ser Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val
        355                 360                 365

Arg Val Leu Gly Leu Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly
    370                 375                 380

Gly Gly Ala Ser Leu Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val
385                 390                 395                 400

Ala Ile Leu Ala Gln
                405


<210> 71
<211> 1398
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1375)
<223> RXA00235

<400> 71
cgaaacaaga ttcgtgcaac aattgggtgt agacgtgatt gaagacattt gatcacgtga 60

ataattctag ttagctccca agttggcata ggaggccaca gtg gct gaa atc atg   115
                                            Val Ala Glu Ile Met
                                              1               5

cac gta ttc gct cgc gaa att ctc gac tcc cgc ggt aac cca acc gtc   163
His Val Phe Ala Arg Glu Ile Leu Asp Ser Arg Gly Asn Pro Thr Val
                 10                  15                  20

gag gca gag gtt ttc ctg gat gac ggt tcc cac ggt gtc gca ggt gtt   211
Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His Gly Val Ala Gly Val
             25                  30                  35

cca tcc ggc gca tcc acc ggc gtc cac gag gct cat gag ctg cgt gac   259
Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala His Glu Leu Arg Asp
         40                  45                  50

ggt ggc gat cgc tac ctg ggc aag ggc gtt ttg aag gca gtt gaa aac   307
Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu Lys Ala Val Glu Asn
     55                  60                  65

gtc aac gaa gaa atc ggc gac gag ctc gct ggc cta gag gct gac gat   355
Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly Leu Glu Ala Asp Asp
 70                  75                  80                  85
```

```
cag cgc ctc atc gac gaa gca atg atc aag ctt gat ggc acc gcc aac   403
Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu Asp Gly Thr Ala Asn
                 90                  95                 100

aag tcc cgc ctg ggt gca aac gca atc ctt ggt gtt tcc atg gct gtt   451
Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly Val Ser Met Ala Val
            105                 110                 115

gca aag gct gct gct gat tcc gca ggc ctc cca ctg ttc cgc tac atc   499
Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro Leu Phe Arg Tyr Ile
        120                 125                 130

ggt gga cca aac gca cac gtt ctt cca gtt cca atg atg aac atc atc   547
Gly Gly Pro Asn Ala His Val Leu Pro Val Pro Met Met Asn Ile Ile
    135                 140                 145

acc ggt ggc gct cac gct gac tcc ggt gtt gac gtt cag gaa ttc atg   595
Thr Gly Gly Ala His Ala Asp Ser Gly Val Asp Val Gln Glu Phe Met
150                 155                 160                 165

atc gct cca atc ggt gca gag acc ttc tct gag gct ctc cgc aac ggc   643
Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu Ala Leu Arg Asn Gly
                170                 175                 180

gcg gag gtc tac cac gca ctg aag tcc gtc atc aag gaa aag ggc ctg   691
Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile Lys Glu Lys Gly Leu
            185                 190                 195

tcc acc gga ctt ggc gat gag ggc ggc ttc gct cct tcc gtc ggc tcc   739
Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala Pro Ser Val Gly Ser
        200                 205                 210

acc cgt gag gct ctt gac ctt atc gtt gag gca atc gag aag gct ggc   787
Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala Ile Glu Lys Ala Gly
    215                 220                 225

ttc acc cca ggc aag gac atc gct ctt gct ctg gac gtt gct tcc tct   835
Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu Asp Val Ala Ser Ser
230                 235                 240                 245

gag ttc ttc aag gac ggc acc tac cac ttc gaa ggt ggc cag cac tcc   883
Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu Gly Gly Gln His Ser
                250                 255                 260

gca gct gag atg gca aac gtt tac gct gag ctc gtt gac gcg tac cca   931
Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu Val Asp Ala Tyr Pro
            265                 270                 275

atc gtc tcc atc gag gac cca ctg cag gaa gat gac tgg gag ggt tac   979
Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp Asp Trp Glu Gly Tyr
        280                 285                 290

acc aac ctc acc gca acc atc ggc gac aag gtt cag atc gtt ggc gac   1027
Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val Gln Ile Val Gly Asp
    295                 300                 305

gac ttc ttc gtc acc aac cct gag cgc ctg aag gag ggc atc gct aag   1075
Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys Glu Gly Ile Ala Lys
310                 315                 320                 325
```

```
aag gct gcc aac tcc atc ctg gtt aag gtg aac cag atc ggt acc ctc   1123
Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn Gln Ile Gly Thr Leu
                330                 335                 340

acc gag acc ttc gac gct gtc gac atg gct cac cgc gca ggc tac acc   1171
Thr Glu Thr Phe Asp Ala Val Asp Met Ala His Arg Ala Gly Tyr Thr
            345                 350                 355

tcc atg atg tcc cac cgt tcc ggt gag acc gag gac acc acc att gct   1219
Ser Met Met Ser His Arg Ser Gly Glu Thr Glu Asp Thr Thr Ile Ala
        360                 365                 370

gac ctc gca gtt gca ctc aac tgt ggc cag atc aag act ggt gct cca   1267
Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile Lys Thr Gly Ala Pro
    375                 380                 385

gca cgt tcc gac cgt gtc gca aag tac aac cag ctt ctc cgc atc gag   1315
Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln Leu Leu Arg Ile Glu
390                 395                 400                 405

cag ctg ctt ggc gac gcc ggc gtc tac gca ggt cgc agc gca ttc cca   1363
Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly Arg Ser Ala Phe Pro
                410                 415                 420

cgc ttt cag ggc taaataaaag cgcttttcga cgc                        1398
Arg Phe Gln Gly
            425
```

<210> 72
<211> 425
<212> PRT
<213> Corynebacterium glutamicum

<400> 72

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Val Ala Glu Ile Met His Val Phe Ala Arg Glu Ile Leu Asp Ser Arg
  1               5                  10                  15

Gly Asn Pro Thr Val Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His
             20                  25                  30

Gly Val Ala Gly Val Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala
         35                  40                  45

His Glu Leu Arg Asp Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu
     50                  55                  60

Lys Ala Val Glu Asn Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly
 65                  70                  75                  80

Leu Glu Ala Asp Asp Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu
                 85                  90                  95

Asp Gly Thr Ala Asn Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly
            100                 105                 110

Val Ser Met Ala Val Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro
        115                 120                 125

Leu Phe Arg Tyr Ile Gly Gly Pro Asn Ala His Val Leu Pro Val Pro
    130                 135                 140
```

```
Met Met Asn Ile Ile Thr Gly Gly Ala His Ala Asp Ser Gly Val Asp
145                 150                 155                 160

Val Gln Glu Phe Met Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu
                165                 170                 175

Ala Leu Arg Asn Gly Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile
            180                 185                 190

Lys Glu Lys Gly Leu Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala
        195                 200                 205

Pro Ser Val Gly Ser Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala
    210                 215                 220

Ile Glu Lys Ala Gly Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu
225                 230                 235                 240

Asp Val Ala Ser Ser Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu
                245                 250                 255

Gly Gly Gln His Ser Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu
            260                 265                 270

Val Asp Ala Tyr Pro Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp
        275                 280                 285

Asp Trp Glu Gly Tyr Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val
    290                 295                 300

Gln Ile Val Gly Asp Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys
305                 310                 315                 320

Glu Gly Ile Ala Lys Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn
                325                 330                 335

Gln Ile Gly Thr Leu Thr Glu Thr Phe Asp Ala Val Asp Met Ala His
            340                 345                 350

Arg Ala Gly Tyr Thr Ser Met Met Ser His Arg Ser Gly Glu Thr Glu
        355                 360                 365

Asp Thr Thr Ile Ala Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile
    370                 375                 380

Lys Thr Gly Ala Pro Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln
385                 390                 395                 400

Leu Leu Arg Ile Glu Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly
                405                 410                 415

Arg Ser Ala Phe Pro Arg Phe Gln Gly
            420                 425
```

<210> 73
<211> 1554
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1531)
<223> RXA01093

<400> 73
cagaggcgta gaacattgtc tgttcacact ctgggtcgca agattcatcg agaattaatg 60

gtagtacctg tggcttgagg gggaatgacg tactaggctt atg ggc gtg gat aga 115
Met Gly Val Asp Arg
1 5

cga act aag att gta tgt acc cta ggc cca gcg gtg gct agt gca gat 163
Arg Thr Lys Ile Val Cys Thr Leu Gly Pro Ala Val Ala Ser Ala Asp
10 15 20

gga att ctg cgt ttg gta gaa gac ggc atg gat gtt gct cgc ctc aac 211
Gly Ile Leu Arg Leu Val Glu Asp Gly Met Asp Val Ala Arg Leu Asn
25 30 35

ttc tcc cat ggt gac cac cca gat cat gag caa aac tac aag tgg gtc 259
Phe Ser His Gly Asp His Pro Asp His Glu Gln Asn Tyr Lys Trp Val
40 45 50

cgc gag gcg gcg gag aag act ggc cgt gca gtc ggt att ctc gca gac 307
Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val Gly Ile Leu Ala Asp
55 60 65

ctc caa gga ccg aag atc cgt ctt ggc cgt ttc act gac ggc gca acc 355
Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe Thr Asp Gly Ala Thr
70 75 80 85

gtg tgg gaa aac ggc gag acc att cgg atc acc gtt gac gat gta gag 403
Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr Val Asp Asp Val Glu
90 95 100

gga acg cac gat cgt gtg tcc acc acc tac aag aat ctg gca aaa gac 451
Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys Asn Leu Ala Lys Asp
105 110 115

gcg aag cca ggc gac cgc ctg ctc gtt gat gac ggc aag gtt ggc ctc 499
Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp Gly Lys Val Gly Leu
120 125 130

gtc tgc gtt tcc gtc gaa ggt aac gac gtc atc tgt gag gtt gtt gag 547
Val Cys Val Ser Val Glu Gly Asn Asp Val Ile Cys Glu Val Val Glu
135 140 145

ggc gga cca gtc tcc aac aac aag ggt gtt tcc ctg cca ggt atg gat 595
Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser Leu Pro Gly Met Asp
150 155 160 165

att tcc gta cct gca ctg tcc gaa aag gat atc cgt gac ctg cgc ttc 643
Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile Arg Asp Leu Arg Phe
170 175 180

gcc ctg aag ctc ggc gtg gac ttt att gca ctg tcc ttc gta cgt tcc 691
Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu Ser Phe Val Arg Ser
185 190 195

cca gca gat gct gaa ctc gtt cac aag atc atg gac gaa gaa ggt cgt 739

```
Pro Ala Asp Ala Glu Leu Val His Lys Ile Met Asp Glu Glu Gly Arg
        200                 205                 210

cgt gtt cct gtg atc gcc aag ctg gaa aag cca gag gct gtc acc tcc   787
Arg Val Pro Val Ile Ala Lys Leu Glu Lys Pro Glu Ala Val Thr Ser
    215                 220                 225

ctc gag cca atc gtg ttg gca ttc gac gcc gtc atg gtt gct cgt ggt   835
Leu Glu Pro Ile Val Leu Ala Phe Asp Ala Val Met Val Ala Arg Gly
230                 235                 240                 245

gac ctc ggc gtt gag gtt cct ctg gag gag gtt cca ctg gtt cag aag   883
Asp Leu Gly Val Glu Val Pro Leu Glu Glu Val Pro Leu Val Gln Lys
                250                 255                 260

cgc gca atc cag att gcc cgt gag aac gca aag cca gtt atc gtg gca   931
Arg Ala Ile Gln Ile Ala Arg Glu Asn Ala Lys Pro Val Ile Val Ala
            265                 270                 275

acc cag atg ctg gat tcc atg att gag aac tcc cgc cca acc cgt gcg   979
Thr Gln Met Leu Asp Ser Met Ile Glu Asn Ser Arg Pro Thr Arg Ala
        280                 285                 290

gaa gct tct gac gtg gca aac gct gtg ctc gat ggc gca gat gct gtc   1027
Glu Ala Ser Asp Val Ala Asn Ala Val Leu Asp Gly Ala Asp Ala Val
    295                 300                 305

atg ctt tct ggt gaa act tca gtg ggc aaa gat ccg cac aac gtt gtg   1075
Met Leu Ser Gly Glu Thr Ser Val Gly Lys Asp Pro His Asn Val Val
310                 315                 320                 325

cgc acc atg tct cgc att gtt cgc ttc gct gaa acc gac ggt cgc gtc   1123
Arg Thr Met Ser Arg Ile Val Arg Phe Ala Glu Thr Asp Gly Arg Val
                330                 335                 340

cca gac ctg acc cac atc cct cgc act aag cgt ggc gtt att tcc tac   1171
Pro Asp Leu Thr His Ile Pro Arg Thr Lys Arg Gly Val Ile Ser Tyr
            345                 350                 355

tct gca cgt gat atc gcc gag cgc ctc aac gct cgt gca ttg gtt gcg   1219
Ser Ala Arg Asp Ile Ala Glu Arg Leu Asn Ala Arg Ala Leu Val Ala
        360                 365                 370

ttc acc acc tct ggt gat acc gca aag cgt gtg gct cgt ctg cac agc   1267
Phe Thr Thr Ser Gly Asp Thr Ala Lys Arg Val Ala Arg Leu His Ser
    375                 380                 385

cac ctg cca ctg ctc gtg ttc act cca aat gag gca gtt cgc tct gag   1315
His Leu Pro Leu Leu Val Phe Thr Pro Asn Glu Ala Val Arg Ser Glu
390                 395                 400                 405

ctg gcg ctg acc tgg ggt gca acc acc ttc ctg tgt cca cct gtc agc   1363
Leu Ala Leu Thr Trp Gly Ala Thr Thr Phe Leu Cys Pro Pro Val Ser
                410                 415                 420

gat acc gat gac atg atg cgc gaa gtc gac cgt gct ctt tta gca atg   1411
Asp Thr Asp Asp Met Met Arg Glu Val Asp Arg Ala Leu Leu Ala Met
            425                 430                 435

cct gag tac aac aag ggt gac atg atg gtt gtt gtt gca ggt tcc cct   1459
Pro Glu Tyr Asn Lys Gly Asp Met Met Val Val Val Ala Gly Ser Pro
```

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        440                 445                 450

cct ggt gtt acc ggt aac acc aac atg att cac gtc cac ctt ctt ggt   1507
Pro Gly Val Thr Gly Asn Thr Asn Met Ile His Val His Leu Leu Gly
    455                 460                 465

gac gac aca agg att gca aag ctc taatcgctta aatctttcaa aaa         1554
Asp Asp Thr Arg Ile Ala Lys Leu
470                 475
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<210> 74
<211> 477
<212> PRT
<213> Corynebacterium glutamicum

<400> 74

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Met Gly Val Asp Arg Arg Thr Lys Ile Val Cys Thr Leu Gly Pro Ala
  1               5                  10                  15

Val Ala Ser Ala Asp Gly Ile Leu Arg Leu Val Glu Asp Gly Met Asp
            20                  25                  30

Val Ala Arg Leu Asn Phe Ser His Gly Asp His Pro Asp His Glu Gln
        35                  40                  45

Asn Tyr Lys Trp Val Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val
    50                  55                  60

Gly Ile Leu Ala Asp Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe
65                  70                  75                  80

Thr Asp Gly Ala Thr Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr
                85                  90                  95

Val Asp Asp Val Glu Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys
            100                 105                 110

Asn Leu Ala Lys Asp Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp
        115                 120                 125

Gly Lys Val Gly Leu Val Cys Val Ser Val Glu Gly Asn Asp Val Ile
    130                 135                 140

Cys Glu Val Val Glu Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser
145                 150                 155                 160

Leu Pro Gly Met Asp Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile
                165                 170                 175

Arg Asp Leu Arg Phe Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu
            180                 185                 190

Ser Phe Val Arg Ser Pro Ala Asp Ala Glu Leu Val His Lys Ile Met
        195                 200                 205

Asp Glu Glu Gly Arg Arg Val Pro Val Ile Ala Lys Leu Glu Lys Pro
    210                 215                 220

Glu Ala Val Thr Ser Leu Glu Pro Ile Val Leu Ala Phe Asp Ala Val
225                 230                 235                 240
```

```
Met Val Ala Arg Gly Asp Leu Gly Val Glu Val Pro Leu Glu Glu Val
                245                 250                 255

Pro Leu Val Gln Lys Arg Ala Ile Gln Ile Ala Arg Glu Asn Ala Lys
            260                 265                 270

Pro Val Ile Val Ala Thr Gln Met Leu Asp Ser Met Ile Glu Asn Ser
        275                 280                 285

Arg Pro Thr Arg Ala Glu Ala Ser Asp Val Ala Asn Ala Val Leu Asp
    290                 295                 300

Gly Ala Asp Ala Val Met Leu Ser Gly Glu Thr Ser Val Gly Lys Asp
305                 310                 315                 320

Pro His Asn Val Val Arg Thr Met Ser Arg Ile Val Arg Phe Ala Glu
                325                 330                 335

Thr Asp Gly Arg Val Pro Asp Leu Thr His Ile Pro Arg Thr Lys Arg
            340                 345                 350

Gly Val Ile Ser Tyr Ser Ala Arg Asp Ile Ala Glu Arg Leu Asn Ala
        355                 360                 365

Arg Ala Leu Val Ala Phe Thr Thr Ser Gly Asp Thr Ala Lys Arg Val
    370                 375                 380

Ala Arg Leu His Ser His Leu Pro Leu Leu Val Phe Thr Pro Asn Glu
385                 390                 395                 400

Ala Val Arg Ser Glu Leu Ala Leu Thr Trp Gly Ala Thr Thr Phe Leu
                405                 410                 415

Cys Pro Pro Val Ser Asp Thr Asp Asp Met Met Arg Glu Val Asp Arg
            420                 425                 430

Ala Leu Leu Ala Met Pro Glu Tyr Asn Lys Gly Asp Met Met Val Val
        435                 440                 445

Val Ala Gly Ser Pro Pro Gly Val Thr Gly Asn Thr Asn Met Ile His
    450                 455                 460

Val His Leu Leu Gly Asp Asp Thr Arg Ile Ala Lys Leu
465                 470                 475
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<210> 75
<211> 1980
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1957)
<223> RXN02675

<400> 75
aagtgtttca ttggaacact tgcgctgcca acttttggt ttacgggcac aatgaaactg 60

ttggatggaa tttagagtgt ttgtagctta aggagctcaa atg aat gag ttt gac 115

```
                                                    Met Asn Glu Phe Asp
                                                      1               5

cag gac att ctc cag gag atc aag act gaa ctc gac gag tta att cta   163
Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu Asp Glu Leu Ile Leu
                10                  15                  20

gaa ctt gat gag gtg aca caa act cac agc gag gcc atc ggg cag gtc   211
Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu Ala Ile Gly Gln Val
            25                  30                  35

tcc cca acc cat tac gtt ggt gcc cgc aac ctc atg cat tac gcg cat   259
Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu Met His Tyr Ala His
        40                  45                  50

ctt cgc acc aaa gac ctc cgt ggc ctg cag caa cgc ctc tcc tct gtg   307
Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln Arg Leu Ser Ser Val
    55                  60                  65

gga gct acc cgc ttg act acc acc gaa cca gca gtg cag gcc cgc ctc   355
Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala Val Gln Ala Arg Leu
70                  75                  80                  85

aag gcc gcc cgc aat gtt atc gga gct ttc gca ggt gaa ggc cca ctt   403
Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala Gly Glu Gly Pro Leu
                90                  95                  100

tat cca ccc tca gat gtc gtc gat gcc ttc gaa gat gcc gat gag att   451
Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu Asp Ala Asp Glu Ile
            105                 110                 115

ctc gac gag cac gcc gaa att ctc ctt ggc gaa ccc cta ccg gat act   499
Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu Pro Leu Pro Asp Thr
        120                 125                 130

cca tcc tgc atc atg gtc acc ctg ccc acc gaa gcc gcc acc gac att   547
Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu Ala Ala Thr Asp Ile
    135                 140                 145

gaa ctt gtc cgt ggc ttc gcc aaa agc ggc atg aat cta gct cgc atc   595
Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met Asn Leu Ala Arg Ile
150                 155                 160                 165

aac tgt gca cac gac gat gaa acc gtc tgg aag cag atg atc gac aac   643
Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys Gln Met Ile Asp Asn
                170                 175                 180

gtc cac acc gtt gca gaa gaa gtt ggc cgg gaa atc cgc gtc agc atg   691
Val His Thr Val Ala Glu Glu Val Gly Arg Glu Ile Arg Val Ser Met
            185                 190                 195

gac ctc gcc gga cca aaa gta cgc acc ggc gaa atc gcc cca ggc gca   739
Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu Ile Ala Pro Gly Ala
        200                 205                 210

gaa gta ggt cgc gca cga gta acc cgc gac gaa acc gga aaa gta ctg   787
Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu Thr Gly Lys Val Leu
    215                 220                 225

acg ccc gca aaa ctg tgg atc acc gcc cac ggc tcc gaa cca gtc cca   835
Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly Ser Glu Pro Val Pro
```

```
230                 235                 240                 245

gcc ccc gaa agc ctg ccc ggt cgc ccc gct ctg ccg att gaa gtc acc   883
Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu Pro Ile Glu Val Thr
                250                 255                 260

cca gaa tgg ttc gac aaa cta gaa atc ggc agc gtc atc aac gtc cca   931
Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser Val Ile Asn Val Pro
            265                 270                 275

gac acc cgc gga tcc cgc cga gca ttc acc gtg acc agg gtt ttt gat   979
Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val Thr Arg Val Phe Asp
        280                 285                 290

ggc gcg gtc ctc gcc gaa ggc cca caa aaa gcc tac atc tcc aac ggc   1027
Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala Tyr Ile Ser Asn Gly
    295                 300                 305

acc ctc ctg gaa cac aac tac gac cgc tcc cgg gtc tac ggc atc ccc   1075
Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg Val Tyr Gly Ile Pro
310                 315                 320                 325

gcc gta gtt cag cgc atc aac ctc aaa gtc ggc gac cgc ctc atc ctt   1123
Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly Asp Arg Leu Ile Leu
                330                 335                 340

acc gac gaa gaa ctc acc tac gat cca tcc ctc gga tcc ggc cgc aca   1171
Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu Gly Ser Gly Arg Thr
            345                 350                 355

cca cgc atc agc tgc acc ctt cca caa gca gtc gat gca att aaa gtc   1219
Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val Asp Ala Ile Lys Val
        360                 365                 370

ggg cac cgc gtg ctt ttc gac gac gga gcc atc gcc gca gtc tgc atc   1267
Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile Ala Ala Val Cys Ile
    375                 380                 385

gac aag acc tcc act gcc gac ggc cac aac gac gta gaa ttg gaa gtc   1315
Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp Val Glu Leu Glu Val
390                 395                 400                 405

acc cac gcc cgc cca caa ggc gta aac ctg gcc gca tac aag gga atc   1363
Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala Ala Tyr Lys Gly Ile
                410                 415                 420

aac ctc cca gac tcc gaa ctt cca ctc cca agc ctc act gaa gaa gac   1411
Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser Leu Thr Glu Glu Asp
            425                 430                 435

ctc caa cac ctg cgc ttt gtc gtc aaa tac gcc gac atc gca gcc atc   1459
Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala Asp Ile Ala Ala Ile
        440                 445                 450

tcc ttc atc cga aac gtc gcc gac gtg gaa tac ctc ctc caa gca ctc   1507
Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr Leu Leu Gln Ala Leu
    455                 460                 465

gcc gac atc gga gat cca gta gcc gtc gaa cgc ctt ggc ctc gtc ctt   1555
Ala Asp Ile Gly Asp Pro Val Ala Val Glu Arg Leu Gly Leu Val Leu
470                 475                 480                 485
```

```
aaa atc gag acc atc cca ggc tac gaa ggc ctc gcc caa atc ctc ctg   1603
Lys Ile Glu Thr Ile Pro Gly Tyr Glu Gly Leu Ala Gln Ile Leu Leu
                490                 495                 500

acc ggc atg cgc cac gaa aac ttc ggc atc atg atc gcc cgc gga gac   1651
Thr Gly Met Arg His Glu Asn Phe Gly Ile Met Ile Ala Arg Gly Asp
            505                 510                 515

ctc gcc gtc gaa ctc ggc ttc gac cgc atg gca gaa gtc ccc caa ctg   1699
Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val Pro Gln Leu
        520                 525                 530

atc atg gcc ctt gcc gaa gcc gcc cac gtc cca acc atc ttg gcc acc   1747
Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile Leu Ala Thr
    535                 540                 545

caa gtc ctg gaa aac atg gcc aaa aac gga ctc cca tct cgc gca gaa   1795
Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser Arg Ala Glu
550                 555                 560                 565

atc acc gac gca gca atg gca ctt cgc gct gaa tgc gtc atg ctg aac   1843
Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val Met Leu Asn
                570                 575                 580

aag gga cca cac atc aac gac gcc atc aag gtc ctc acc gaa atg agc   1891
Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr Glu Met Ser
            585                 590                 595

cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg ctg cgc aag   1939
Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu Leu Arg Lys
        600                 605                 610

gtg aag agc tgg gaa gag taactcacaa aggcgattgg cgt                 1980
Val Lys Ser Trp Glu Glu
    615
```

<210> 76
<211> 619
<212> PRT
<213> Corynebacterium glutamicum

<400> 76

```
Met Asn Glu Phe Asp Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu
  1               5                  10                  15

Asp Glu Leu Ile Leu Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu
             20                  25                  30

Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu
         35                  40                  45

Met His Tyr Ala His Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln
     50                  55                  60

Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala
 65                  70                  75                  80

Val Gln Ala Arg Leu Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala
                 85                  90                  95
```

```
Gly Glu Gly Pro Leu Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu
            100                 105                 110

Asp Ala Asp Glu Ile Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu
        115                 120                 125

Pro Leu Pro Asp Thr Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu
    130                 135                 140

Ala Ala Thr Asp Ile Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met
145                 150                 155                 160

Asn Leu Ala Arg Ile Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys
                165                 170                 175

Gln Met Ile Asp Asn Val His Thr Val Ala Glu Glu Val Gly Arg Glu
            180                 185                 190

Ile Arg Val Ser Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu
        195                 200                 205

Ile Ala Pro Gly Ala Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu
    210                 215                 220

Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly
225                 230                 235                 240

Ser Glu Pro Val Pro Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu
                245                 250                 255

Pro Ile Glu Val Thr Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser
            260                 265                 270

Val Ile Asn Val Pro Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val
        275                 280                 285

Thr Arg Val Phe Asp Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala
    290                 295                 300

Tyr Ile Ser Asn Gly Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg
305                 310                 315                 320

Val Tyr Gly Ile Pro Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly
                325                 330                 335

Asp Arg Leu Ile Leu Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu
            340                 345                 350

Gly Ser Gly Arg Thr Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val
        355                 360                 365

Asp Ala Ile Lys Val Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile
    370                 375                 380

Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp
385                 390                 395                 400

Val Glu Leu Glu Val Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala
                405                 410                 415
```

```
Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser
            420                 425                 430

Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala
        435                 440                 445

Asp Ile Ala Ala Ile Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr
    450                 455                 460

Leu Leu Gln Ala Leu Ala Asp Ile Gly Asp Pro Val Ala Val Glu Arg
465                 470                 475                 480

Leu Gly Leu Val Leu Lys Ile Glu Thr Ile Pro Gly Tyr Glu Gly Leu
                485                 490                 495

Ala Gln Ile Leu Leu Thr Gly Met Arg His Glu Asn Phe Gly Ile Met
            500                 505                 510

Ile Ala Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala
        515                 520                 525

Glu Val Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro
    530                 535                 540

Thr Ile Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu
545                 550                 555                 560

Pro Ser Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu
                565                 570                 575

Cys Val Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val
            580                 585                 590

Leu Thr Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg
        595                 600                 605

Leu Leu Leu Arg Lys Val Lys Ser Trp Glu Glu
    610                 615
```

<210> 77
<211> 386
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(363)
<223> FRXA02675

<400> 77

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atc ctc atg acc ggc atg cgc cac gaa aac ttc ggc atc atg atc gcc   48
Ile Leu Met Thr Gly Met Arg His Glu Asn Phe Gly Ile Met Ile Ala
  1               5                  10                  15

cgc gga gac ctc gcc gtc gaa ctc ggc ttc gac cgc atg gca gaa gtc   96
Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val
            20                  25                  30

ccc caa ctg atc atg gcc ctt gca gaa gcc gcc cac gtc cca acc atc   144
Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile
```

```
          35                  40                  45

ttg gcc acc caa gtc ctg gaa aac atg gcc aaa aac gga ctc cca tct   192
Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser
     50                  55                  60

cgc gca gaa atc acc gac gca gca atg gca ctt cgc gct gaa tgc gtc   240
Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val
 65                  70                  75                  80

atg ctg aac aag gga cca cac atc aac gac gcc atc aag gtc ctc acc   288
Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr
                85                  90                  95

gaa atg agc cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg   336
Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu
            100                 105                 110

ctg cgc aag gtg aag agc tgg gaa gag taactcacaa aggcgattgg        383
Leu Arg Lys Val Lys Ser Trp Glu Glu
        115                 120

cgt                                                              386
```

<210> 78
<211> 121
<212> PRT
<213> Corynebacterium glutamicum

<400> 78

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Ile Leu Met Thr Gly Met Arg His Glu Asn Phe Gly Ile Met Ile Ala
  1               5                  10                  15

Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val
             20                  25                  30

Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile
         35                  40                  45

Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser
     50                  55                  60

Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val
 65                  70                  75                  80

Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr
                85                  90                  95

Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu
            100                 105                 110

Leu Arg Lys Val Lys Ser Trp Glu Glu
        115                 120
```

<210> 79
<211> 1522
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1522)
<223> FRXA02695

<400> 79
aagtgtttca ttggaacact tgcgctgcca acttttttggt ttacgggcac aatgaaactg 60

ttggatggaa tttagagtgt ttgtagctta aggagctcaa atg aat gag ttt gac 115
Met Asn Glu Phe Asp
1 5

cag gac att ctc cag gag atc aag act gaa ctc gac gag tta att cta 163
Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu Asp Glu Leu Ile Leu
10 15 20

gaa ctt gat gag gtg aca caa act cac agc gag gcc atc ggg cag gtc 211
Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu Ala Ile Gly Gln Val
25 30 35

tcc cca acc cat tac gtt ggt gcc cgc aac ctc atg cat tac gcg cat 259
Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu Met His Tyr Ala His
40 45 50

ctt cgc acc aaa gac ctc cgt ggc ctg cag caa cgc ctc tcc tct gtg 307
Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln Arg Leu Ser Ser Val
55 60 65

gga gct acc cgc ttg act acc acc gaa cca gca gtg cag gcc cgc ctc 355
Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala Val Gln Ala Arg Leu
70 75 80 85

aag gcc gcc cgc aat gtt atc gga gct ttc gca ggt gaa ggc cca ctt 403
Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala Gly Glu Gly Pro Leu
90 95 100

tat cca ccc tca gat gtc gtc gat gcc ttc gaa gat gcc gat gag att 451
Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu Asp Ala Asp Glu Ile
105 110 115

ctc gac gag cac gcc gaa att ctc ctt ggc gaa ccc cta ccg gat act 499
Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu Pro Leu Pro Asp Thr
120 125 130

cca tcc tgc atc atg gtc acc ctg ccc acc gaa gcc gcc acc gac att 547
Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu Ala Ala Thr Asp Ile
135 140 145

gaa ctt gtc cgt ggc ttc gcc aaa agc ggc atg aat cta gct cgc atc 595
Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met Asn Leu Ala Arg Ile
150 155 160 165

aac tgt gca cac gac gat gaa acc gtc tgg aag cag atg atc gac aac 643
Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys Gln Met Ile Asp Asn
170 175 180

gtc cac acc gtt gca gaa gaa gtt ggc cgg gaa atc cgc gtc agc atg 691
Val His Thr Val Ala Glu Glu Val Gly Arg Glu Ile Arg Val Ser Met
185 190 195

gac ctc gcc gga cca aaa gta cgc acc ggc gaa atc gcc cca ggc gca 739

```
Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu Ile Ala Pro Gly Ala
        200                 205                 210

gaa gta ggt cgc gca cga gta acc cgc gac gaa acc gga aaa gta ctg   787
Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu Thr Gly Lys Val Leu
    215                 220                 225

acg ccc gca aaa ctg tgg atc acc gcc cac ggc tcc gaa cca gtc cca   835
Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly Ser Glu Pro Val Pro
230                 235                 240                 245

gcc ccc gaa agc ctg ccc ggt cgc ccc gct ctg ccg att gaa gtc acc   883
Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu Pro Ile Glu Val Thr
                250                 255                 260

cca gaa tgg ttc gac aaa cta gaa atc ggc agc gtc atc aac gtc cca   931
Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser Val Ile Asn Val Pro
            265                 270                 275

gac acc cgc gga tcc cgc cga gca ttc acc gtg acc agg gtt ttt gat   979
Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val Thr Arg Val Phe Asp
        280                 285                 290

ggc gcg gtc ctc gcc gaa ggc cca caa aaa gcc tac atc tcc aac ggc   1027
Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala Tyr Ile Ser Asn Gly
    295                 300                 305

acc ctc ctg gaa cac aac tac gac cgc tcc cgg gtc tac ggc atc ccc   1075
Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg Val Tyr Gly Ile Pro
310                 315                 320                 325

gcc gta gtt cag cgc atc aac ctc aaa gtc ggc gac cgc ctc atc ctt   1123
Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly Asp Arg Leu Ile Leu
                330                 335                 340

acc gac gaa gaa ctc acc tac gat cca tcc ctc gga tcc ggc cgc aca   1171
Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu Gly Ser Gly Arg Thr
            345                 350                 355

cca cgc atc agc tgc acc ctt cca caa gca gtc gat gca att aaa gtc   1219
Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val Asp Ala Ile Lys Val
        360                 365                 370

ggg cac cgc gtg ctt ttc gac gac gga gcc atc gcc gca gtc tgc atc   1267
Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile Ala Ala Val Cys Ile
    375                 380                 385

gac aag acc tcc act gcc gac ggc cac aac gac gta gaa ttg gaa gtc   1315
Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp Val Glu Leu Glu Val
390                 395                 400                 405

acc cac gcc cgc cca caa ggc gta aac ctg gcc gca tac aag gga atc   1363
Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala Ala Tyr Lys Gly Ile
                410                 415                 420

aac ctc cca gac tcc gaa ctt cca ctc cca agc ctc act gaa gaa gac   1411
Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser Leu Thr Glu Glu Asp
            425                 430                 435

ctc caa cac ctg cgc ttt gtc gtc aaa tac gcc gac atc gca gcc atc   1459
Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala Asp Ile Ala Ala Ile
```

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        440                 445                 450

tcc ttc atc cga aac gtc gcc gac gtg gaa tac ctc ctc caa gca ctc   1507
Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr Leu Leu Gln Ala Leu
    455                 460                 465

gcc gac atc gga gat                                               1522
Ala Asp Ile Gly Asp
470


<210> 80
<211> 474
<212> PRT
<213> Corynebacterium glutamicum

<400> 80
Met Asn Glu Phe Asp Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu
  1               5                  10                  15

Asp Glu Leu Ile Leu Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu
             20                  25                  30

Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu
         35                  40                  45

Met His Tyr Ala His Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln
     50                  55                  60

Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala
 65                  70                  75                  80

Val Gln Ala Arg Leu Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala
                 85                  90                  95

Gly Glu Gly Pro Leu Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu
            100                 105                 110

Asp Ala Asp Glu Ile Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu
        115                 120                 125

Pro Leu Pro Asp Thr Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu
    130                 135                 140

Ala Ala Thr Asp Ile Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met
145                 150                 155                 160

Asn Leu Ala Arg Ile Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys
                165                 170                 175

Gln Met Ile Asp Asn Val His Thr Val Ala Glu Glu Val Gly Arg Glu
            180                 185                 190

Ile Arg Val Ser Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu
        195                 200                 205

Ile Ala Pro Gly Ala Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu
    210                 215                 220

Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly
225                 230                 235                 240
```

```
Ser Glu Pro Val Pro Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu
                245                 250                 255

Pro Ile Glu Val Thr Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser
            260                 265                 270

Val Ile Asn Val Pro Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val
        275                 280                 285

Thr Arg Val Phe Asp Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala
    290                 295                 300

Tyr Ile Ser Asn Gly Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg
305                 310                 315                 320

Val Tyr Gly Ile Pro Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly
                325                 330                 335

Asp Arg Leu Ile Leu Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu
            340                 345                 350

Gly Ser Gly Arg Thr Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val
        355                 360                 365

Asp Ala Ile Lys Val Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile
    370                 375                 380

Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp
385                 390                 395                 400

Val Glu Leu Glu Val Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala
                405                 410                 415

Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser
            420                 425                 430

Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala
        435                 440                 445

Asp Ile Ala Ala Ile Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr
    450                 455                 460

Leu Leu Gln Ala Leu Ala Asp Ile Gly Asp
465                 470
```

<210> 81
<211> 2022
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1999)
<223> RXA00682

<400> 81
ataggcacct tcgatttcag ctcaatcacc gtcgcaatga ccggcacgaa gtaaaaccac 60

cgcatctttt cgtcgaaaag catctaaaag gagtttgacc atg gct aat aaa tct 115

```
                                                    Met Ala Asn Lys Ser
                                                      1               5

ttc ccc aag ccc tcc gat ctt cca gtg ccc aag ggc gct gaa ggt tgg   163
Phe Pro Lys Pro Ser Asp Leu Pro Val Pro Lys Gly Ala Glu Gly Trp
                 10                  15                  20

gaa gat ctg tac ccg tac tac ctc gtt ttc caa gac aag ctc atg gat   211
Glu Asp Leu Tyr Pro Tyr Tyr Leu Val Phe Gln Asp Lys Leu Met Asp
             25                  30                  35

caa gag aat gag aaa ttc tgg ttc tgc gat tca cag cac tgg cca act   259
Gln Glu Asn Glu Lys Phe Trp Phe Cys Asp Ser Gln His Trp Pro Thr
         40                  45                  50

gtg ttc aag cct ttt gaa act atc ggt ggt gaa ttc gct gta aag tgc   307
Val Phe Lys Pro Phe Glu Thr Ile Gly Gly Glu Phe Ala Val Lys Cys
     55                  60                  65

ctc ggc caa tac aac gct cgg cat ttg atg atc ccg aat gcc aat ggc   355
Leu Gly Gln Tyr Asn Ala Arg His Leu Met Ile Pro Asn Ala Asn Gly
 70                  75                  80                  85

atc gag ttc cgc gtg cat ctg gga tac ctc tat atg tcc cct att cca   403
Ile Glu Phe Arg Val His Leu Gly Tyr Leu Tyr Met Ser Pro Ile Pro
                 90                  95                 100

gtg cct gaa gat cag att gcg gaa cgc gtc ccc atg ttc cag gaa cgc   451
Val Pro Glu Asp Gln Ile Ala Glu Arg Val Pro Met Phe Gln Glu Arg
             105                 110                 115

atc acg cac tac ttc caa aac tgg gag cca atg ctg gca aat tgg aag   499
Ile Thr His Tyr Phe Gln Asn Trp Glu Pro Met Leu Ala Asn Trp Lys
         120                 125                 130

gag cga gta tta gga acc atc aat gag ctg gaa tct cta gaa ttc aag   547
Glu Arg Val Leu Gly Thr Ile Asn Glu Leu Glu Ser Leu Glu Phe Lys
     135                 140                 145

cca ctg cct gac tac gtg cct atc gat gat att gtc tcc gga aaa gcc   595
Pro Leu Pro Asp Tyr Val Pro Ile Asp Asp Ile Val Ser Gly Lys Ala
150                 155                 160                 165

aaa gac ggc acc gaa gta ctc atg gaa aac ttc gat cgg ctc att cag   643
Lys Asp Gly Thr Glu Val Leu Met Glu Asn Phe Asp Arg Leu Ile Gln
                 170                 175                 180

ctc gcc tac caa aac tgg caa tac cac ttt gag ttc ctc aac ttg ggt   691
Leu Ala Tyr Gln Asn Trp Gln Tyr His Phe Glu Phe Leu Asn Leu Gly
             185                 190                 195

tac atc gct tac cta gat ttc ttc aat ttc tgc aag gaa gtc ttc cca   739
Tyr Ile Ala Tyr Leu Asp Phe Phe Asn Phe Cys Lys Glu Val Phe Pro
         200                 205                 210

gat atc cct gat caa tca att tcg atg atg gtt cag ggc gtg gat atg   787
Asp Ile Pro Asp Gln Ser Ile Ser Met Met Val Gln Gly Val Asp Met
     215                 220                 225

gag ctg ttc cgc ccc gat gat gaa cta aag att ctg gca cag cta gcg   835
Glu Leu Phe Arg Pro Asp Asp Glu Leu Lys Ile Leu Ala Gln Leu Ala
```

```
230                 235                 240                 245

gtc gac ctt ggc ctg caa act cac ttt gcc aac ccg gat gat ccg caa   883
Val Asp Leu Gly Leu Gln Thr His Phe Ala Asn Pro Asp Asp Pro Gln
                250                 255                 260

gct acc ttg gct gct atc gca aag gca gaa ggc ggc gcg aca tgg ata   931
Ala Thr Leu Ala Ala Ile Ala Lys Ala Glu Gly Gly Ala Thr Trp Ile
            265                 270                 275

gcg cgc tgg gaa gaa gca caa gat ccg tgg ttc aac ttc acc gtc ggt   979
Ala Arg Trp Glu Glu Ala Gln Asp Pro Trp Phe Asn Phe Thr Val Gly
        280                 285                 290

aat ggc ttc tac ggt cac gat aaa tac tgg atc gag cac ctg gaa ctt   1027
Asn Gly Phe Tyr Gly His Asp Lys Tyr Trp Ile Glu His Leu Glu Leu
    295                 300                 305

cca ctg ggg tac atc gcg gat tac atc cgc cgc cta gat gaa ggc caa   1075
Pro Leu Gly Tyr Ile Ala Asp Tyr Ile Arg Arg Leu Asp Glu Gly Gln
310                 315                 320                 325

acc atc tcc cgc ccg aaa gat gaa ctc atc gca gaa aag gaa cgc gtg   1123
Thr Ile Ser Arg Pro Lys Asp Glu Leu Ile Ala Glu Lys Glu Arg Val
                330                 335                 340

gtg gaa gaa tac cgc gac ctt ttg gat gga gaa caa ctc gcg cag ttt   1171
Val Glu Glu Tyr Arg Asp Leu Leu Asp Gly Glu Gln Leu Ala Gln Phe
            345                 350                 355

gat gct aaa tgc ggc ctc gct gct act gca tac ccc tat gtg gaa aac   1219
Asp Ala Lys Cys Gly Leu Ala Ala Thr Ala Tyr Pro Tyr Val Glu Asn
        360                 365                 370

cat aac ttc tac atc gag cac tgg acc atg tca gta ttt tgg cgc aaa   1267
His Asn Phe Tyr Ile Glu His Trp Thr Met Ser Val Phe Trp Arg Lys
    375                 380                 385

gta cgc gaa ctt tcc cgc act ctc cag ggc tac ggt ttc tgg gag aac   1315
Val Arg Glu Leu Ser Arg Thr Leu Gln Gly Tyr Gly Phe Trp Glu Asn
390                 395                 400                 405

gag gat gac atg ttg tac ctc aac cgc act gaa gtc cgc gat gtc ctc   1363
Glu Asp Asp Met Leu Tyr Leu Asn Arg Thr Glu Val Arg Asp Val Leu
                410                 415                 420

ttc gac ctg gct act gcg tgg ggt gtc ggc gca ccc ggt ggt cca att   1411
Phe Asp Leu Ala Thr Ala Trp Gly Val Gly Ala Pro Gly Gly Pro Ile
            425                 430                 435

ggc acg atc att tgg ccg gaa gaa att gag cga aga aaa gca att gtc   1459
Gly Thr Ile Ile Trp Pro Glu Glu Ile Glu Arg Arg Lys Ala Ile Val
        440                 445                 450

acc gct ttg aaa act gcc cga cca gcg cca gct ctt aac act cct cca   1507
Thr Ala Leu Lys Thr Ala Arg Pro Ala Pro Ala Leu Asn Thr Pro Pro
    455                 460                 465

gag tcc atc acc gaa cct ttc acc cgc atg ctc tgg gga atc acc acc   1555
Glu Ser Ile Thr Glu Pro Phe Thr Arg Met Leu Trp Gly Ile Thr Thr
470                 475                 480                 485
```

```
gaa cag gtg caa tca tgg ttg ggc aat gac gag gat gcc gaa gaa gga   1603
Glu Gln Val Gln Ser Trp Leu Gly Asn Asp Glu Asp Ala Glu Glu Gly
                490                 495                 500

acc ctt aaa ggc atg gct gca tcc cct ggt gtg gtg gaa ggc tac gct   1651
Thr Leu Lys Gly Met Ala Ala Ser Pro Gly Val Val Glu Gly Tyr Ala
            505                 510                 515

cga gta att ctc agc gca gat gac ctt tca gaa atc cag cag gat gaa   1699
Arg Val Ile Leu Ser Ala Asp Asp Leu Ser Glu Ile Gln Gln Asp Glu
        520                 525                 530

atc ctc gtt gcc cct gta aca gca cct tct tgg ggc cca atc ttt ggc   1747
Ile Leu Val Ala Pro Val Thr Ala Pro Ser Trp Gly Pro Ile Phe Gly
    535                 540                 545

aaa atc aag gca aca gtc act gat att ggt ggc atg atg agc cat gct   1795
Lys Ile Lys Ala Thr Val Thr Asp Ile Gly Gly Met Met Ser His Ala
550                 555                 560                 565

gcg atc gtg tgc cgc gaa tac ggc ttg ccg gct gtt act gga act ggc   1843
Ala Ile Val Cys Arg Glu Tyr Gly Leu Pro Ala Val Thr Gly Thr Gly
                570                 575                 580

gct gca tcc acc acc atc aaa acc ggc gat tac ctc aag gtc gat gga   1891
Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr Leu Lys Val Asp Gly
            585                 590                 595

acc aag ggc aag gtt gtc att gtt gat cca gat gcg cca cgc atc gaa   1939
Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp Ala Pro Arg Ile Glu
        600                 605                 610

gga ccc ggc gcg cac agc cat gcg cac tca gta gca gca cat ggg gtg   1987
Gly Pro Gly Ala His Ser His Ala His Ser Val Ala Ala His Gly Val
    615                 620                 625

gat aca cat gcc tagtccacgc actgttctta tca                        2022
Asp Thr His Ala
630
```

<210> 82
<211> 633
<212> PRT
<213> Corynebacterium glutamicum

<400> 82

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Met Ala Asn Lys Ser Phe Pro Lys Pro Ser Asp Leu Pro Val Pro Lys
  1               5                  10                  15

Gly Ala Glu Gly Trp Glu Asp Leu Tyr Pro Tyr Tyr Leu Val Phe Gln
             20                  25                  30

Asp Lys Leu Met Asp Gln Glu Asn Glu Lys Phe Trp Phe Cys Asp Ser
         35                  40                  45

Gln His Trp Pro Thr Val Phe Lys Pro Phe Glu Thr Ile Gly Gly Glu
     50                  55                  60

Phe Ala Val Lys Cys Leu Gly Gln Tyr Asn Ala Arg His Leu Met Ile
```

65 70 75 80

Pro Asn Ala Asn Gly Ile Glu Phe Arg Val His Leu Gly Tyr Leu Tyr
85 90 95

Met Ser Pro Ile Pro Val Pro Glu Asp Gln Ile Ala Glu Arg Val Pro
100 105 110

Met Phe Gln Glu Arg Ile Thr His Tyr Phe Gln Asn Trp Glu Pro Met
115 120 125

Leu Ala Asn Trp Lys Glu Arg Val Leu Gly Thr Ile Asn Glu Leu Glu
130 135 140

Ser Leu Glu Phe Lys Pro Leu Pro Asp Tyr Val Pro Ile Asp Asp Ile
145 150 155 160

Val Ser Gly Lys Ala Lys Asp Gly Thr Glu Val Leu Met Glu Asn Phe
165 170 175

Asp Arg Leu Ile Gln Leu Ala Tyr Gln Asn Trp Gln Tyr His Phe Glu
180 185 190

Phe Leu Asn Leu Gly Tyr Ile Ala Tyr Leu Asp Phe Phe Asn Phe Cys
195 200 205

Lys Glu Val Phe Pro Asp Ile Pro Asp Gln Ser Ile Ser Met Met Val
210 215 220

Gln Gly Val Asp Met Glu Leu Phe Arg Pro Asp Asp Glu Leu Lys Ile
225 230 235 240

Leu Ala Gln Leu Ala Val Asp Leu Gly Leu Gln Thr His Phe Ala Asn
245 250 255

Pro Asp Asp Pro Gln Ala Thr Leu Ala Ala Ile Ala Lys Ala Glu Gly
260 265 270

Gly Ala Thr Trp Ile Ala Arg Trp Glu Glu Ala Gln Asp Pro Trp Phe
275 280 285

Asn Phe Thr Val Gly Asn Gly Phe Tyr Gly His Asp Lys Tyr Trp Ile
290 295 300

Glu His Leu Glu Leu Pro Leu Gly Tyr Ile Ala Asp Tyr Ile Arg Arg
305 310 315 320

Leu Asp Glu Gly Gln Thr Ile Ser Arg Pro Lys Asp Glu Leu Ile Ala
325 330 335

Glu Lys Glu Arg Val Val Glu Glu Tyr Arg Asp Leu Leu Asp Gly Glu
340 345 350

Gln Leu Ala Gln Phe Asp Ala Lys Cys Gly Leu Ala Ala Thr Ala Tyr
355 360 365

Pro Tyr Val Glu Asn His Asn Phe Tyr Ile Glu His Trp Thr Met Ser
370 375 380

Val Phe Trp Arg Lys Val Arg Glu Leu Ser Arg Thr Leu Gln Gly Tyr
385 390 395 400

```
Gly Phe Trp Glu Asn Glu Asp Asp Met Leu Tyr Leu Asn Arg Thr Glu
                405                 410                 415

Val Arg Asp Val Leu Phe Asp Leu Ala Thr Ala Trp Gly Val Gly Ala
            420                 425                 430

Pro Gly Gly Pro Ile Gly Thr Ile Ile Trp Pro Glu Glu Ile Glu Arg
        435                 440                 445

Arg Lys Ala Ile Val Thr Ala Leu Lys Thr Ala Arg Pro Ala Pro Ala
    450                 455                 460

Leu Asn Thr Pro Pro Glu Ser Ile Thr Glu Pro Phe Thr Arg Met Leu
465                 470                 475                 480

Trp Gly Ile Thr Thr Glu Gln Val Gln Ser Trp Leu Gly Asn Asp Glu
                485                 490                 495

Asp Ala Glu Glu Gly Thr Leu Lys Gly Met Ala Ala Ser Pro Gly Val
            500                 505                 510

Val Glu Gly Tyr Ala Arg Val Ile Leu Ser Ala Asp Asp Leu Ser Glu
        515                 520                 525

Ile Gln Gln Asp Glu Ile Leu Val Ala Pro Val Thr Ala Pro Ser Trp
    530                 535                 540

Gly Pro Ile Phe Gly Lys Ile Lys Ala Thr Val Thr Asp Ile Gly Gly
545                 550                 555                 560

Met Met Ser His Ala Ala Ile Val Cys Arg Glu Tyr Gly Leu Pro Ala
                565                 570                 575

Val Thr Gly Thr Gly Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr
            580                 585                 590

Leu Lys Val Asp Gly Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp
        595                 600                 605

Ala Pro Arg Ile Glu Gly Pro Gly Ala His Ser His Ala His Ser Val
    610                 615                 620

Ala Ala His Gly Val Asp Thr His Ala
625                 630
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<210> 83
<211> 1215
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1192)
<223> RXA00683

<400> 83
ggacaaagct atcgggttcc gggagaacct ctccttccgc gtccccactt ctgttcccgt 60

gacttggaac gcttaacgct ttattaaata aggagacacc atg acc aac agt ttg 115

```
                                                    Met Thr Asn Ser Leu
                                                      1               5

aac atc ccg ttt gtc cag cgc ttc gat gaa ggc ctg gat cct gtt cta   163
Asn Ile Pro Phe Val Gln Arg Phe Asp Glu Gly Leu Asp Pro Val Leu
                 10                  15                  20

gaa gta ctc ggt ggc aag ggc gct tca cta gtc acc atg aca gat gct   211
Glu Val Leu Gly Gly Lys Gly Ala Ser Leu Val Thr Met Thr Asp Ala
             25                  30                  35

gga atg ccc gtt cca cct gga ttt gtg gtc act act gcc agc ttt gat   259
Gly Met Pro Val Pro Pro Gly Phe Val Val Thr Thr Ala Ser Phe Asp
         40                  45                  50

gaa ttc atc cgt gaa gca ggg gtt gct gaa cac atc gat aaa ttc cta   307
Glu Phe Ile Arg Glu Ala Gly Val Ala Glu His Ile Asp Lys Phe Leu
     55                  60                  65

aac gat ctc gat gca gaa gat gtt aag gaa gtg gat cga gtt tct gcg   355
Asn Asp Leu Asp Ala Glu Asp Val Lys Glu Val Asp Arg Val Ser Ala
 70                  75                  80                  85

atc atc cgc gat gag ctg tgc agt ctt gac gtt cca gag aat gct cgt   403
Ile Ile Arg Asp Glu Leu Cys Ser Leu Asp Val Pro Glu Asn Ala Arg
                 90                  95                 100

ttc gca gtg cac cag gct tat cgc gat ctc atg gaa cga tgc ggt ggc   451
Phe Ala Val His Gln Ala Tyr Arg Asp Leu Met Glu Arg Cys Gly Gly
            105                 110                 115

gac gtc ccg gtt gct gtc cgg tca tcg gcc act gcc gaa gat ctg ccc   499
Asp Val Pro Val Ala Val Arg Ser Ser Ala Thr Ala Glu Asp Leu Pro
        120                 125                 130

gat gct tcc ttc gca ggg caa cag gac acc tat ctg tgg caa gtc ggt   547
Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr Leu Trp Gln Val Gly
    135                 140                 145

ttg agc gct gtc act gaa cac atc cgt aaa tgc tgg gct tcg ctg ttc   595
Leu Ser Ala Val Thr Glu His Ile Arg Lys Cys Trp Ala Ser Leu Phe
150                 155                 160                 165

act tcc cgt gcc att atc tac cgt ctg aaa aac aac atc ccc aat gag   643
Thr Ser Arg Ala Ile Ile Tyr Arg Leu Lys Asn Asn Ile Pro Asn Glu
                170                 175                 180

ggc ctc tcc atg gcg gta gtt gtt caa aaa atg gtc aac tct cgt gtc   691
Gly Leu Ser Met Ala Val Val Val Gln Lys Met Val Asn Ser Arg Val
            185                 190                 195

gca ggc gtg gca atc act atg aat cct tcc aac ggc gac cgc tcg aag   739
Ala Gly Val Ala Ile Thr Met Asn Pro Ser Asn Gly Asp Arg Ser Lys
        200                 205                 210

atc acc atc gat tcc tca tgg ggt gtt ggt gaa atg gtg gtc tca ggt   787
Ile Thr Ile Asp Ser Ser Trp Gly Val Gly Glu Met Val Val Ser Gly
    215                 220                 225

gaa gtg aca cca gac aat atc ttg ctg gac aag atc acg ctg cag gtt   835
Glu Val Thr Pro Asp Asn Ile Leu Leu Asp Lys Ile Thr Leu Gln Val
```

```
230                 235                 240                 245

gtc tcc gaa cac att gga agc aaa cac gct gaa ctc atc ccc gat gcc   883
Val Ser Glu His Ile Gly Ser Lys His Ala Glu Leu Ile Pro Asp Ala
                250                 255                 260

acc agt gga agc ctc gtg gaa aag ccc gtt gat gaa gaa cgc gca aac   931
Thr Ser Gly Ser Leu Val Glu Lys Pro Val Asp Glu Glu Arg Ala Asn
            265                 270                 275

cgc cgc agt ctg act gat gag gaa atg ctc gct gtg gca caa atg gct   979
Arg Arg Ser Leu Thr Asp Glu Glu Met Leu Ala Val Ala Gln Met Ala
        280                 285                 290

aag cgt gca gaa aaa cac tac aag tgc cca caa gat atc gaa tgg gcg   1027
Lys Arg Ala Glu Lys His Tyr Lys Cys Pro Gln Asp Ile Glu Trp Ala
    295                 300                 305

ctg gac gct gat ctg cca gat gga gaa aac ctt ctg tta ttg caa tcc   1075
Leu Asp Ala Asp Leu Pro Asp Gly Glu Asn Leu Leu Leu Leu Gln Ser
310                 315                 320                 325

cgc ccg gaa act atc cac tcc aac ggt gtg aag aag gaa acc cca act   1123
Arg Pro Glu Thr Ile His Ser Asn Gly Val Lys Lys Glu Thr Pro Thr
                330                 335                 340

ccg cag gct gcc aaa acc ata ggc acc ttc gat ttc agc tca atc acc   1171
Pro Gln Ala Ala Lys Thr Ile Gly Thr Phe Asp Phe Ser Ser Ile Thr
            345                 350                 355

gtc gca atg acc ggc acg aag taaaaccacc gcatcttttc gtc            1215
Val Ala Met Thr Gly Thr Lys
        360
```

<210> 84
<211> 364
<212> PRT
<213> Corynebacterium glutamicum

<400> 84

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Met Thr Asn Ser Leu Asn Ile Pro Phe Val Gln Arg Phe Asp Glu Gly
  1               5                  10                  15

Leu Asp Pro Val Leu Glu Val Leu Gly Gly Lys Gly Ala Ser Leu Val
             20                  25                  30

Thr Met Thr Asp Ala Gly Met Pro Val Pro Pro Gly Phe Val Val Thr
         35                  40                  45

Thr Ala Ser Phe Asp Glu Phe Ile Arg Glu Ala Gly Val Ala Glu His
     50                  55                  60

Ile Asp Lys Phe Leu Asn Asp Leu Asp Ala Glu Asp Val Lys Glu Val
 65                  70                  75                  80

Asp Arg Val Ser Ala Ile Ile Arg Asp Glu Leu Cys Ser Leu Asp Val
                 85                  90                  95

Pro Glu Asn Ala Arg Phe Ala Val His Gln Ala Tyr Arg Asp Leu Met
            100                 105                 110
```

```
Glu Arg Cys Gly Gly Asp Val Pro Val Ala Val Arg Ser Ser Ala Thr
        115                 120                 125

Ala Glu Asp Leu Pro Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr
    130                 135                 140

Leu Trp Gln Val Gly Leu Ser Ala Val Thr Glu His Ile Arg Lys Cys
145                 150                 155                 160

Trp Ala Ser Leu Phe Thr Ser Arg Ala Ile Ile Tyr Arg Leu Lys Asn
                165                 170                 175

Asn Ile Pro Asn Glu Gly Leu Ser Met Ala Val Val Val Gln Lys Met
            180                 185                 190

Val Asn Ser Arg Val Ala Gly Val Ala Ile Thr Met Asn Pro Ser Asn
        195                 200                 205

Gly Asp Arg Ser Lys Ile Thr Ile Asp Ser Ser Trp Gly Val Gly Glu
    210                 215                 220

Met Val Val Ser Gly Glu Val Thr Pro Asp Asn Ile Leu Leu Asp Lys
225                 230                 235                 240

Ile Thr Leu Gln Val Val Ser Glu His Ile Gly Ser Lys His Ala Glu
                245                 250                 255

Leu Ile Pro Asp Ala Thr Ser Gly Ser Leu Val Glu Lys Pro Val Asp
            260                 265                 270

Glu Glu Arg Ala Asn Arg Arg Ser Leu Thr Asp Glu Glu Met Leu Ala
        275                 280                 285

Val Ala Gln Met Ala Lys Arg Ala Glu Lys His Tyr Lys Cys Pro Gln
    290                 295                 300

Asp Ile Glu Trp Ala Leu Asp Ala Asp Leu Pro Asp Gly Glu Asn Leu
305                 310                 315                 320

Leu Leu Leu Gln Ser Arg Pro Glu Thr Ile His Ser Asn Gly Val Lys
                325                 330                 335

Lys Glu Thr Pro Thr Pro Gln Ala Ala Lys Thr Ile Gly Thr Phe Asp
            340                 345                 350

Phe Ser Ser Ile Thr Val Ala Met Thr Gly Thr Lys
        355                 360


<210> 85
<211> 1860
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1837)
<223> RXN00635

<400> 85
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ctggcaggcg ggcgaagcgt ggcaacaact ggaatttaag agcacaattg aagtcgcacc 60

aagttaggca acacaatagc cataacgttg aggagttcag atg gca cac agc tac   115
                                              Met Ala His Ser Tyr
                                                1               5

gca gaa caa tta att gac act ttg gaa gct caa ggt gtg aag cga att   163
Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile
                 10                  15                  20

tat ggt ttg gtg ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc   211
Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg
             25                  30                  35

caa tca gat att gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg   259
Gln Ser Asp Ile Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala
         40                  45                  50

ttt gca gcc ggt gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt   307
Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys
     55                  60                  65

gct gct tct tgt ggt cct gga aac aca cac ctg att cag ggt ctt tat   355
Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr
 70                  75                  80                  85

gat tcg cat cga aat ggt gcg aag gtg ttg gcc atc gct agc cat att   403
Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile
                 90                  95                 100

ccg agt gcc cag att ggt tcg acg ttc ttc cag gaa acg cat ccg gag   451
Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu
            105                 110                 115

att ttg ttt aag gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt   499
Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly
        120                 125                 130

gag cag ggt gaa cgc att ttg cat cac gcg att cag tcc acc atg gcg   547
Glu Gln Gly Glu Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala
    135                 140                 145

ggt aaa ggt gtg tcg gtg gta gtg att cct ggt gat atc gct aag gaa   595
Gly Lys Gly Val Ser Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu
150                 155                 160                 165

gac gca ggt gac ggt act tat tcc aat tcc act att tct tct ggc act   643
Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr
                170                 175                 180

cct gtg gtg ttc ccg gat cct act gag gct gca gcg ctg gtg gag gcg   691
Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala
            185                 190                 195

att aac aac gct aag tct gtc act ttg ttc tgc ggt gcg ggc gtg aag   739
Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys
        200                 205                 210

aat gct cgc gcg cag gtg ttg gag ttg gcg gag aag att aaa tca ccg   787
Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro
    215                 220                 225
```

```
atc ggg cat gcg ctg ggt ggt aag cag tac atc cag cat gag aat ccg   835
Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro
230                 235                 240                 245

ttt gag gtc ggc atg tct ggc ctg ctt ggt tac ggc gcc tgc gtg gat   883
Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp
                250                 255                 260

gcg tcc aat gag gcg gat ctg ctg att cta ttg ggt acg gat ttc cct   931
Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro
            265                 270                 275

tat tct gat ttc ctt cct aaa gac aac gtt gcc cag gtg gat atc aac   979
Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn
        280                 285                 290

ggt gcg cac att ggt cga cgt acc acg gtg aag tat ccg gtg acc ggt   1027
Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly
    295                 300                 305

gat gtt gct gca aca atc gaa aat att ttg cct cat gtg aag gaa aaa   1075
Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys
310                 315                 320                 325

aca gat cgt tcc ttc ctt gat cgg atg ctc aag gca cac gag cgt aag   1123
Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys
                330                 335                 340

ttg agc tcg gtg gta gag acg tac aca cat aac gtc gag aag cat gtg   1171
Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val
            345                 350                 355

cct att cac cct gaa tac gtt gcc tct att ttg aac gag ctg gcg gat   1219
Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp
        360                 365                 370

aag gat gcg gtg ttt act gtg gat acc ggc atg tgc aat gtg tgg cat   1267
Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His
    375                 380                 385

gcg agg tac atc gag aat ccg gag gga acg cgc gac ttt gtg ggt tca   1315
Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg Asp Phe Val Gly Ser
390                 395                 400                 405

ttc cgc cac ggc acg atg gct aat gcg ttg cct cat gcg att ggt gcg   1363
Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala
                410                 415                 420

caa agt gtt gat cga aac cgc cag gtg atc gcg atg tgt ggc gat ggt   1411
Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly
            425                 430                 435

ggt ttg ggc atg ctg ctg ggt gag ctt ctg acc gtt aag ctg cac caa   1459
Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln
        440                 445                 450

ctt ccg ctg aag gct gtg gtg ttt aac aac agt tct ttg ggc atg gtg   1507
Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val
    455                 460                 465
```

```
aag ttg gag atg ctc gtg gag gga cag cca gaa ttt ggt act gac cat   1555
Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His
470                 475                 480                 485

gag gaa gtg aat ttc gca gag att gcg gcg gct gcg ggt atc aaa tcg   1603
Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala Ala Gly Ile Lys Ser
                490                 495                 500

gta cgc atc acc gat ccg aag aaa gtt cgc gag cag cta gct gag gca   1651
Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala
            505                 510                 515

ttg gca tat cct gga cct gta ctg atc gat atc gtc acg gat cct aat   1699
Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn
        520                 525                 530

gcg ctg tcg atc cca cca acc atc acg tgg gaa cag gtc atg gga ttc   1747
Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe
    535                 540                 545

agc aag gcg gcc acc cga acc gtc ttt ggt gga gga gta gga gcg atg   1795
Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met
550                 555                 560                 565

atc gat ctg gcc cgt tcg aac ata agg aat att cct act cca           1837
Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile Pro Thr Pro
                570                 575

tgatgattga tacacctgct gtt                                        1860
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<210> 86
<211> 579
<212> PRT
<213> Corynebacterium glutamicum

<400> 86

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Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln
  1               5                  10                  15

Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
             20                  25                  30

Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
         35                  40                  45

Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
     50                  55                  60

Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
 65                  70                  75                  80

Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
                 85                  90                  95

Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
            100                 105                 110

Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
        115                 120                 125
```

```
Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
    130                 135                 140

Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly
145                 150                 155                 160

Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
                165                 170                 175

Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
            180                 185                 190

Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys
        195                 200                 205

Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
    210                 215                 220

Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile
225                 230                 235                 240

Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
                245                 250                 255

Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu
            260                 265                 270

Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
        275                 280                 285

Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
    290                 295                 300

Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
305                 310                 315                 320

His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
                325                 330                 335

Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
            340                 345                 350

Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
        355                 360                 365

Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
    370                 375                 380

Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
385                 390                 395                 400

Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
                405                 410                 415

His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
            420                 425                 430

Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
        435                 440                 445

Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
```

```
    450                 455                 460

Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
465                 470                 475                 480

Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
                485                 490                 495

Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
            500                 505                 510

Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
        515                 520                 525

Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
    530                 535                 540

Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
545                 550                 555                 560

Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
                565                 570                 575

Pro Thr Pro
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<210> 87
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (88)..(552)
<223> FRXA02807

<400> 87

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aaagcgtggc aacaactgga atttaagagc acaattgaag tcgcaccaag ttaggcaaca 60

caatagccat aacgttgagg agttcagatg gca cac agc tac gca gaa caa tta  114
                              Met Ala His Ser Tyr Ala Glu Gln Leu
                                1               5

att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg   162
Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val
 10                  15                  20                  25

ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att   210
Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile
                 30                  35                  40

gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg ttt gca gcc ggt   258
Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly
             45                  50                  55

gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt   306
Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys
         60                  65                  70

ggt cct gga aac aca cac ctg att cag ggt ctt tat gat tcg cat cga   354
```

```
Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr Asp Ser His Arg
     75                  80                  85

aat ggt gcg aag gtg ttg gcc atc gct agc cat att ccg agt gcc cag   402
Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile Pro Ser Ala Gln
 90                  95                 100                 105

att ggt tcg acg ttc ttc cag gaa acg cat ccg gag att ttg ttt aag   450
Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu Ile Leu Phe Lys
                110                 115                 120

gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt gag cag ggt gaa   498
Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly Glu Gln Gly Glu
            125                 130                 135

cgc att ttg cat cac gcg att cag tcc acc atg gcg ggt aaa ggt gtg   546
Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala Gly Lys Gly Val
        140                 145                 150

tcg gtg                                                          552
Ser Val
    155


<210> 88
<211> 155
<212> PRT
<213> Corynebacterium glutamicum

<400> 88
Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln
  1               5                  10                  15

Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
             20                  25                  30

Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
         35                  40                  45

Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
     50                  55                  60

Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
 65                  70                  75                  80

Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
                85                  90                  95

Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
            100                 105                 110

Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
        115                 120                 125

Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
    130                 135                 140

Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val
145                 150                 155
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<210> 89
<211> 944
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(921)
<223> FRXA00635

<400> 89

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ggt acg gat ttc cct tat tct gat ttc ctt cct aaa gac aac gtt gcc   48
Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
  1               5                  10                  15

cag gtg gat atc aac ggt gcg cac att ggt cga cgt acc acg gtg aag   96
Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
             20                  25                  30

tat ccg gtg acc ggt gat gtt gct gca aca atc gaa aat att ttg cct   144
Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
         35                  40                  45

cat gtg aag gaa aaa aca gat cgt tcc ttc ctt gat cgg atg ctc aag   192
His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
     50                  55                  60

gca cac gag cgt aag ttg agc tcg gtg gta gag acg tac aca cat aac   240
Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
 65                  70                  75                  80

gtc gag aag cat gtg cct att cac cct gaa tac gtt gcc tct att ttg   288
Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
                 85                  90                  95

aac gag ctg gcg gat aag gat gcg gtg ttt act gtg gat acc ggc atg   336
Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
            100                 105                 110

tgc aat gtg tgg cat gcg agg tac atc gag aat ccg gag gga acg cgc   384
Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
        115                 120                 125

gac ttt gtg ggt tca ttc cgc cac ggc acg atg gct aat gcg ttg cct   432
Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
    130                 135                 140

cat gcg att ggt gcg caa agt gtt gat cga aac cgc cag gtg atc gcg   480
His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
145                 150                 155                 160

atg tgt ggc gat ggt ggt ttg ggc atg ctg ctg ggt gag ctt ctg acc   528
Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
                165                 170                 175

gtt aag ctg cac caa ctt ccg ctg aag gct gtg gtg ttt aac aac agt   576
Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
            180                 185                 190

tct ttg ggc atg gtg aag ttg gag atg ctc gtg gag gga cag cca gaa   624
Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
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        195                 200                 205

ttt ggt act gac cat gag gaa gtg aat ttc gca gag att gcg gcg gct   672
Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
    210                 215                 220

gcg ggt atc aaa tcg gta cgc atc acc gat ccg aag aaa gtt cgc gag   720
Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
225                 230                 235                 240

cag cta gct gag gca ttg gca tat cct gga cct gta ctg atc gat atc   768
Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
                245                 250                 255

gtc acg gat cct aat gcg ctg tcg atc cca cca acc atc acg tgg gaa   816
Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
            260                 265                 270

cag gtc atg gga ttc agc aag gcg gcc acc cga acc gtc ttt ggt gga   864
Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
        275                 280                 285

gga gta gga gcg atg atc gat ctg gcc cgt tcg aac ata agg aat att   912
Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
    290                 295                 300

cct act cca tgatgattga tacacctgct gtt                            944
Pro Thr Pro
305
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<210> 90
<211> 307
<212> PRT
<213> Corynebacterium glutamicum

<400> 90

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Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
  1               5                  10                  15

Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
            20                  25                  30

Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
        35                  40                  45

His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
    50                  55                  60

Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
65                  70                  75                  80

Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
                85                  90                  95

Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
            100                 105                 110

Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
        115                 120                 125
```

```
Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
    130                 135                 140

His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
145                 150                 155                 160

Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
                165                 170                 175

Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
            180                 185                 190

Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
        195                 200                 205

Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
    210                 215                 220

Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
225                 230                 235                 240

Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
                245                 250                 255

Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
            260                 265                 270

Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
        275                 280                 285

Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
    290                 295                 300

Pro Thr Pro
305
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<210> 91
<211> 954
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(931)
<223> RXN03044

<400> 91

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tacgccaccc acggcaaggc catgattccg ctgtacatct tctactcgat gttcgggatt 60

ccagcgcacc ggtgactcca tctgggcagc agccgatcag atg gca cgt ggc ttc   115
                                            Met Ala Arg Gly Phe
                                              1               5

ctc ttg ggc gct acc gca ggt cgc acc acc ctg acc ggt gaa ggc ctc   163
Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu
                 10                  15                  20

cag cac atg gat gga cac tcc cct gtc ttg gct tcc acc aac gag ggt   211
Gln His Met Asp Gly His Ser Pro Val Leu Ala Ser Thr Asn Glu Gly
             25                  30                  35
```

```
gtc gag acc tac gac cca tcc ttt gcg tac gag atc gca cac ctg gtt   259
Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val
         40                  45                  50

cac cgt ggc atc gac cgc atg tac ggc cca ggc aag ggt gaa gat gtt   307
His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val
     55                  60                  65

atc tac tac atc acc atc tac aac gag cca acc cca cag cca gct gag   355
Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu
 70                  75                  80                  85

cca gaa gga ctg gac gta gaa ggc ctg cac aag ggc atc tac ctc tac   403
Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr
                 90                  95                 100

tcc cgc ggt gaa ggc acc ggc cat gag gca aac atc ttg gct tcc ggt   451
Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn Ile Leu Ala Ser Gly
            105                 110                 115

gtt ggt atg cag tgg gct ctc aag gct gca tcc atc ctt gag gct gac   499
Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser Ile Leu Glu Ala Asp
        120                 125                 130

tac gga gtt cgt gcc aac att tac tcc gct act tct tgg gtt aac ttg   547
Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr Ser Trp Val Asn Leu
    135                 140                 145

gct cgc gat ggc gct gct cgt aac aag gca cag ctg cgc aac cca ggt   595
Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln Leu Arg Asn Pro Gly
150                 155                 160                 165

gca gat gct ggc gag gca ttc gta acc acc cag ctg aag cag acc tcc   643
Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln Leu Lys Gln Thr Ser
                170                 175                 180

ggc cca tac gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag   691
Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln
            185                 190                 195

atc cgt gaa tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc   739
Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly
        200                 205                 210

ttc ggt ttc tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc   787
Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile
    215                 220                 225

gac gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa   835
Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu
230                 235                 240                 245

ggc aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag   883
Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys
                250                 255                 260

ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa   931
Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
            265                 270                 275
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taaatcacct caagggacag ata 954

<210> 92
<211> 277
<212> PRT
<213> Corynebacterium glutamicum

<400> 92
Met Ala Arg Gly Phe Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu
1 5 10 15

Thr Gly Glu Gly Leu Gln His Met Asp Gly His Ser Pro Val Leu Ala
20 25 30

Ser Thr Asn Glu Gly Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu
35 40 45

Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly
50 55 60

Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr
65 70 75 80

Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys
85 90 95

Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn
100 105 110

Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser
115 120 125

Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr
130 135 140

Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln
145 150 155 160

Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln
165 170 175

Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr
180 185 190

Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val
195 200 205

Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg
210 215 220

Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn
225 230 235 240

Ser Leu Ala Arg Glu Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala
245 250 255

Ala Glu Lys Phe Lys Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro
260 265 270

Asn Ala Pro Glu Glu

275

<210> 93
<211> 302
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(279)
<223> FRXA02852

<400> 93
gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag atc cgt gaa 48
Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
1 5 10 15

tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc ttc ggt ttc 96
Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
20 25 30

tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag 144
Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
35 40 45

tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc 192
Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
50 55 60

gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat 240
Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
65 70 75 80

cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct 289
Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
85 90

caagggacag ata 302

<210> 94
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 94
Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
1 5 10 15

Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
20 25 30

Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
35 40 45

Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
50 55 60

Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
65 70 75 80

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Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
                 85                  90


<210> 95
<211> 954
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(931)
<223> FRXA00268

<400> 95
tacgccaccc acggcaaggc catgattccg ctgtacatct tctactcgat gttcgggatt 60

ccagcgcacc ggtgactcca tttgggcagc agccgatcag atg gca cgt ggc ttc   115
                                              Met Ala Arg Gly Phe
                                                1               5

ttt ttg ggc gct acc gca ggt cgc acc acc ttg acc ggt gaa ggc ctc   163
Phe Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu
                10                  15                  20

cag cac atg gat gga cac tcc cct gtt ttg gct tcc acc aac gag ggt   211
Gln His Met Asp Gly His Ser Pro Val Leu Ala Ser Thr Asn Glu Gly
            25                  30                  35

gtc gag acc tac gac cca tcc ttt gcg tac gag atc gca cac ctg gtt   259
Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val
        40                  45                  50

cac cgt ggc atc gac cgc atg tac ggc cca ggc aag ggt gaa gat gtt   307
His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val
    55                  60                  65

atc tac tac atc acc atc tac aac gag cca acc cca cag cca gct gag   355
Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu
70                  75                  80                  85

cca gaa gga ctg gac gta gaa ggc ctg cac aag ggc atc tac ctc tac   403
Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr
                90                  95                  100

tcc cgc ggt gaa ggc acc ggc cat gag gca aac atc ttg gct tcc ggt   451
Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn Ile Leu Ala Ser Gly
            105                 110                 115

gtt ggt atg cag tgg gct ctc aag gct gca tcc atc ctt gag gct gac   499
Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser Ile Leu Glu Ala Asp
        120                 125                 130

tac gga gtt cgt gcc aac att tac tcc gct act tct tgg gtt aac ttg   547
Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr Ser Trp Val Asn Leu
    135                 140                 145

gct cgc gat ggc gct gct cgt aac aag gca cag ctg cgc aac cca ggt   595
Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln Leu Arg Asn Pro Gly
150                 155                 160                 165
```

```
gca gat gct ggc gag gca ttc gta acc acc cag ctg aag cag acc tcc   643
Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln Leu Lys Gln Thr Ser
                170                 175                 180

ggc cca tac gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag   691
Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln
            185                 190                 195

atc cgt gaa tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc   739
Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly
        200                 205                 210

ttc ggt ttc tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc   787
Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile
    215                 220                 225

gac gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa   835
Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu
230                 235                 240                 245

ggc aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag   883
Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys
                250                 255                 260

ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa   931
Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
            265                 270                 275

taaatcacct caagggacag ata                                        954
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<210> 96
<211> 277
<212> PRT
<213> Corynebacterium glutamicum

<400> 96

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Met Ala Arg Gly Phe Phe Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu
  1               5                  10                  15

Thr Gly Glu Gly Leu Gln His Met Asp Gly His Ser Pro Val Leu Ala
             20                  25                  30

Ser Thr Asn Glu Gly Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu
         35                  40                  45

Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly
     50                  55                  60

Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr
 65                  70                  75                  80

Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys
                 85                  90                  95

Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn
            100                 105                 110

Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser
        115                 120                 125
```

```
Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr
    130                 135                 140

Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln
145                 150                 155                 160

Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln
                165                 170                 175

Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr
            180                 185                 190

Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val
        195                 200                 205

Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg
    210                 215                 220

Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn
225                 230                 235                 240

Ser Leu Ala Arg Glu Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala
                245                 250                 255

Ala Glu Lys Phe Lys Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro
            260                 265                 270

Asn Ala Pro Glu Glu
        275


<210> 97
<211> 508
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> RXN03086

<400> 97
ttcgtgcact tcggcgtgtc acaattaggt acgaccaaga atgggaccgg gaaaccggga 60

cgtataaacg aaataaaaca ttccaacagg aggtgtggaa atg gcc gat caa gca   115
                                            Met Ala Asp Gln Ala
                                              1               5

aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc   163
Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
                 10                  15                  20

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac   211
Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
             25                  30                  35

gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa   259
Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
         40                  45                  50
```

```
cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag   307
Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
     55                  60                  65

cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att   355
Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile
 70                  75                  80                  85

cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag   403
Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys
                 90                  95                 100

cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc   451
Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg
            105                 110                 115

gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca   499
Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala
        120                 125                 130

ggc gca gcc                                                       508
Gly Ala Ala
    135
```

<210> 98
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 98

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Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn
  1               5                  10                  15

Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
             20                  25                  30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
         35                  40                  45

Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
     50                  55                  60

Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
 65                  70                  75                  80

Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
                 85                  90                  95

Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
            100                 105                 110

Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His
        115                 120                 125

Ile Ser Thr Tyr Ala Gly Ala Ala
    130                 135
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<210> 99
<211> 508

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> FRXA02887

<400> 99
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cgtataaacg aaataaaaca ttccaacagg aggtgtggaa atg gcc gat caa gca 115
Met Ala Asp Gln Ala
1 5

aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
10 15 20

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
25 30 35

gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
40 45 50

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
55 60 65

cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att 355
Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile
70 75 80 85

cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag 403
Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys
90 95 100

cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc 451
Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg
105 110 115

gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca 499
Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala
120 125 130

ggc gca gcc 508
Gly Ala Ala
135

<210> 100
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 100
Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn
1 5 10 15

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Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
            20                  25                  30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
        35                  40                  45

Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
    50                  55                  60

Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
65                  70                  75                  80

Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
                85                  90                  95

Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
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Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His
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Ile Ser Thr Tyr Ala Gly Ala Ala
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Asp Leu Asp Gly Phe Arg Gln Glu Val Ser Arg Glu Gln Gly Gly Ile
  1               5                  10                  15

ccg tcc tac cct cac cca cac ggt atg aag gac ttc tgg gag ttc cca   96
Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
            20                  25                  30

act gtg tcc atg ggt ctt ggc cca atg gat gcc att tac cag gca cgt   144
Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
        35                  40                  45

ttc aac cgc tac ctc gaa aac cgt ggc atc aag gac acc tct gac cag   192
Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
    50                  55                  60

cac gtc tgg gcc ttc ctt ggc gac ggc gaa atg gac gag cca gaa tca   240
His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
65                  70                  75                  80

cgt ggt ctc atc cag cag gct gca ctg aac aac ctg gac aac ctg acc   288
Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
                85                  90                  95

ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt   336
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